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(54) **Title:** CELL CYCLE PROGRESSION PROTEINS

(57) **Abstract:** Polynucleotides encoding a number of *Drosophila* gene products are provided. Polynucleotide probes derived from these nucleotide sequences, polypeptides encoded by the polynucleotides and antibodies that bind to the polypeptides are also provided.

CELL CYCLE PROGRESSION PROTEINS

The present invention relates to a number of genes implicated in the processes of cell cycle progression, including mitosis and meiosis.

We have now identified a large number of genes in *Drosophila*, mutations in which disrupt cell cycle progression, for example the processes of mitosis and/or meiosis. We have determined the phenotypes of these mutations and recovered nucleotide sequences associated with the corresponding genes. Many of these nucleotide sequences correspond to protein open reading frames (ORFs) present in the *Drosophila* genome.

Accordingly the present invention provides in one aspect a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

There is provided, according to another aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

We provide, according to yet a further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide

sequences set out in Examples 15 to 19 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 15 to 19 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

As a further aspect of the present invention, there is provided a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 20 to 30 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

We provide, according to a yet further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

The present invention, in a further aspect, provides a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof; (c)

polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of the above aspects of the invention.

The present invention also provides a polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a homologue, variant, derivative or fragment thereof.

Preferably the polypeptide is encoded by a cDNA sequence obtainable from a eukaryotic cDNA library, preferably a metazoan cDNA library (such as insect or mammalian) said DNA sequence comprising a DNA sequence being selectively detectable with a *Drosophila* nucleotide sequence as shown in any one of Examples 1 to 70.

The term "selectively detectable" means that the cDNA used as a probe is used under conditions where a target cDNA of the invention is found to hybridize to the probe at a level significantly above background. The background hybridization may occur because of other cDNAs present in the cDNA library. In this event background implies a level of signal generated by interaction between the probe and a non-specific cDNA member of the library which is less than 10 fold, preferably less than 100 fold as intense as the specific interaction observed with the target cDNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with ^{32}P. Suitable conditions may be found by reference to the Examples, as well as in the detailed description below.

A polynucleotide encoding a polypeptide of the invention is also provided.

The present invention further provides a vector comprising a polynucleotide of the invention, for example an expression vector comprising a polynucleotide of the invention

operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.

Also provided is an antibody capable of binding a polypeptide of the invention.

In a further aspect the present invention provides a method for detecting the presence or absence of a polynucleotide of the invention in a biological sample which method comprises: (a) bringing the biological sample containing DNA or RNA into contact with a probe comprising a nucleotide of the invention under hybridising conditions; and (b) detecting any duplex formed between the probe and nucleic acid in the sample.

In another aspect the invention provides a method for detecting a polypeptide of the invention present in a biological sample which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

Knowledge of the genes involved in cell cycle progression allows the development of therapeutic agents for the treatment of medical conditions associated with aberrant cell cycle progression. Accordingly, the present invention provides a polynucleotide of the invention for use in therapy. The present invention also provides a polypeptide of the invention for use in therapy. The present invention further provides an antibody of the invention for use in therapy.

In a specific embodiment, the present invention provides a method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of a polynucleotide, polypeptide and/or antibody of the invention.

The present invention also provides the use of a polypeptide of the invention in a method of identifying a substance capable of affecting the function of the corresponding

gene. For example, in one embodiment the present invention provides the use of a polypeptide of the invention in an assay for identifying a substance capable of inhibiting cell cycle progression. The substance may inhibit any of the steps or stages in the cell cycle, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, and cytokinesis functions. For example, possible functions of genes of the invention for which it may be desired to identify substances which affect such functions include chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation, microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In a further aspect the present invention provides a method for identifying a substance capable of binding to a polypeptide of the invention, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.

In an additional aspect, the invention provides kits comprising polynucleotides, polypeptides or antibodies of the invention and methods of using such kits in diagnosing the presence of absence of polynucleotides and polypeptides of the invention including deleterious mutant forms.

Also provided is a substance identified by the above methods of the invention. Such substances may be used in a method of therapy, such as in a method of affecting cell cycle progression, for example mitosis and/or meiosis.

The invention also provides a process comprising the steps of: (a) performing one of the above methods; and (b) preparing a quantity of those one or more substances identified as being capable of binding to a polypeptide of the invention.

Also provided is a process comprising the steps of: (a) performing one of the above methods; and (b) preparing a pharmaceutical composition comprising one or more substances identified as being capable of binding to a polypeptide of the invention.

We further provide a method for identifying a substance capable of modulating the function of a polypeptide of the invention or a polypeptide encoded by a polynucleotide of the invention, the method comprising the steps of: incubating the polypeptide with a candidate substance and determining whether activity of the polypeptide is thereby modulated.

A substance identified by a method or assay according to any of the above methods or processes is also provided, as is the use of such a substance in a method of inhibiting the function of a polypeptide. Use of such a substance in a method of regulating a cell division cycle function is also provided.

DETAILED DESCRIPTION OF THE INVENTION

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA and immunology, which are within the capabilities of a person of ordinary skill in the art. Such techniques are explained in the literature. See, for example, J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Books 1-3, Cold Spring Harbor Laboratory Press; Ausubel, F. M. et al. (1995 and periodic supplements; *Current Protocols in Molecular Biology*, ch. 9, 13, and 16, John Wiley & Sons, New York, N.Y.); B. Roe, J. Crabtree, and A. Kahn, 1996, *DNA Isolation and Sequencing: Essential Techniques*, John Wiley & Sons; J. M. Polak and James O'D. McGee, 1990, *In Situ Hybridization: Principles and Practice*; Oxford University Press; M. J. Gait (Editor), 1984, *Oligonucleotide Synthesis: A Practical Approach*, Irl Press; and, D.

M. J. Lilley and J. E. Dahlberg, 1992, *Methods of Enzymology: DNA Structure Part A: Synthesis and Physical Analysis of DNA* Methods in Enzymology, Academic Press. Each of these general texts is herein incorporated by reference.

Preferably, the polypeptides and polynucleotides of the invention are such that they give rise to or are associated with defined phenotypes when mutated.

For example, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to complete cytokinesis; such polypeptides and polynucleotides are conveniently categorised as "Category 1". Phenotypes associated with Category 1 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: cytokinesis defect (polyploidy); Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects.(Seg-01/62); Meiotic defects in testis: cytokinesis defects, abnormal spindles.(Ab-02/12); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, high polyploidy); Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant; Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis:segregation defect, cytokinesis defect(Ck-09/32); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, very high polyploidy); Mitotic defects in brain: cytokinesis defect(very high polyploidy); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic: Ck05/07); Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy); Mitotic defects in brain: cytokinesis defect (very high polyploidy, chromosomes entangled?); Mitotic defects in brain: cytokinesis defect (very high polyploidy; Meiotic defects in testis: cytokinesis defects (Ck-04/06) `; Female sterile (anaphase bridges, lagging chromosomes); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects:(mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: cytokinesis defects(Ck-06/09); Meiotic defects in testis: segregation defects, cytokinesis defect(Ck-07/35); Meiotic defects in testis: cytokinesis defects.

Alternatively, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to enter M-phase; such polypeptides and polynucleotides are conveniently categorised as "Category 2". Phenotypes associated with Category 2 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Meiotic defects in testis: no division(no meiosis); Mitotic defects in brain: no mitosis; Meiotic defects in testis: segregation defects, meiotic failure(Mf-07/75); Meiotic defects in testis: segregation defects, meiotic failure(Mf-05/31); Meiotic defects in testis: cytokinesis defects, meiotic failure(Mf-02/15).

Mutations in the polypeptides and polynucleotides of the invention may be associated with a metaphase arrest phenotype ("Category 3"). Phenotypes associated with Category 3 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: prometaphase arrest (overcondensation, polyploidy, scattered chromosomes with bipolar spindle); Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest (Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle); Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle); Mitotic defects in brain: prometaphase arrest; Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: metaphase arrest.(overcondensation, polyploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest (overcondensation, metaphase with bipolar spindle; Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29); Meiotic defects in testis: cytokinesis defects,abnormal spindles.(Ab-01/03); Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles (mitotic: High mitotic index, meiotic: Ab-08/24); Mitotic defects in brain: metaphase arrest(overcondensation, few anaphases, some polyploids); Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar spindle);

Mitotic defects in brain: metaphase arrest(condensation, no polyploidy, no anaphases, metaphase with bipolar spindle).

Mutations in Category 4 polypeptides and polynucleotides of the invention may be associated with an anaphase defect phenotype; phenotypes associated with Category 4 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes); Meiotic defects in testis: segregation defects; Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect; Mitotic defects in brain: anaphase defects(overcondensation, anaphase bridge, metaphase with swollen chromosomes and bipolar spindle); Mitotic defects in brain: Anaphase defects. (overcondensation, aneuploidy, some lagging chromosomes and breaks); Meiotic defects in testis: segregation defects; Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/17); Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/18); Meiotic defects in testis: cytokinesis defects, segregation defects (seg-01/01); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects Polyploidy, no overcondensation Pl-01/10; Meiotic defects in testis: segregation defects, abnormal spindles. (Ab-03/30); Mitotic defects in brain: anaphase defects (weak, higher condensation, some polyploidy, fewer anaphases, polyploids with monopolar spindles); Mitotic defects in brain: anaphase defects (overcondensation, polyplody (with overcondensation), few anaphases, metaphase with bipolar spindle); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: segregation defects,multipolar spindles(Mul-02/22); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-04/26); Meiotic defects in testis: cytokinesis defects,abnormal spindles (Ab-16/13); Mitotic defects in brain: anaphase defects. Meiotic defects in testis: segregation defects, abnormal spindles (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20); Meiotic defects in testis: segregation defects; Meiotic defects in testis: no division (no meiosis); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-12/48); Meiotic defects in testis: segregation defects, multipolar spindles(mitotic: High polyploids, no diploids, higher mitotic index Meiotic: Mul-02/59); Meiotic defects in testis: segregation defect; Meiotic defects in testis: segregation defects,abnormal spindles

(meiotic: Ab-08/42); Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02; Mitotic defects in brain: anaphase defects; Meiotic defects in testis: cytokinesis defects,abnormal spindles(Ab-01/04); Meiotic defects in testis: segregation defects(overcondensation, fewer anaphases); Mitotic defects in brain:(some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle).

A fifth category ("Category 5") of polypeptides and polynucleotides of the invention are associated with the presence of small imaginal discs (block to proliferation). Phenotypes associated with Category 5 polypeptides and polynucleotides include any one or more of the following, singly or in combination: 2nd chromosome, small imaginal discs.

The polypeptides and polynucleotides of the invention may also be categorised according to their function, or their putative function.

For example, the polypeptides described here preferably comprise, and the polynucleotides described here are ones which preferably encode polypeptides comprising, any one or more of the following: a CBP activator protein; a CCR4-associated regulator of polymerase II transcription; a CTP synthase (CTPS); a Cyclin specific ubiquitin conjugating enzyme; a DNA packaging protein; a DNA repair protein; a DNA-binding protein involved in chromosomal organisation; a DNase IV; a EIF4G2 translation initiation factor; a eukaryotic translation initiation factor 6; a Ecdysone-induced protein 78C; a Egf2 translation factor; a G protein-coupled receptor kinase 7; a GTPase exchange factor; a phosphatidylinositol transfer protein beta isoform; a His-rich protein; a Lk6 kinase; a MAP kinase; a MAP kinase interacting kinase 1; a N-arginine dibasic convertase; a Phosphatidylinositol transfer protein; a RIP protein kinase; a RNA binding motif, single stranded interacting protein; a RNA binding protein; a RYKreceptor tyrosine kinase; a Ribosomal protein L1; a selenide,water dikinase 1; a selenium donor protein 1; a selenophosphate synthetase 1; a Sqv-7-like protein; a sugar modification protein; a protein involved in cytokinesis and signalling; a TEK tyrosine kinase; a Translation elongation

factor; a UDP-galactose transporter; a v-erba related protein; a WD40 protein; a brahma protein; a calcium binding protein; a cell adhesion protein; a chaperone; a chromodomain helicase DNA binding protein; a chromodomain-helicase-DNA-binding protein; a coiled coil protein with ubiquitin like domain; a component of the 19S proteasome regulatory particle; a couch potato RNA binding protein; a cytidine 5-prime triphosphate synthetasea; a cytoskeletal structural protein; a death domain containing protein; a developmentally expressed in axons of the CNS; a diacylglycerol-activated/phosholipid dependent protein kinase C inhibitor; a diazepam binding inhibitor; a diphosphate kinase; a dodecasattelite DNA binding protein; a doughnut protein tyrosine kinase; an elongation factor 2; a endoplasmic reticulum ATPase; a eukaryotic translation initiation factor 4E binding protein 2; a factor involved in axon guidance; a fatty-acid-Coenzyme A ligase; a flap structure-specific endonuclease 1; a protein involved in the formation of the contractile ring and the initiation of cytokinesis; a glucose-6-phosphate transporter; a glycoprotein glucosyltransferase; a growth factor; a transmembrane receptor protein tyrosine kinase involved in cell growth and maintenance; a guanyl-nucleotide exchange factor involved in signal transduction; a heat shock protein; a helicase; a high density lipoprotein binding protein; a histone acetyl transferase transcriptional activator; a histone acetyltransferase; a histone acetyltransferase GCN5; a protein involved in development of the abdomen (embryos); a protein involved in the development of the imaginal discs (larvae or pupae); a kinesin like protein 67a; a ligand-dependent nuclear receptor; a ligand-dependent nuclear receptor; a lola-like specific RNA polymerase II transcription factor; a matrix associated protein; a membrane glycoprotein; a mitotic heterochromatin fragment clone CH(2)6; a motor protein; a motor protein involved in cytoskeleton organization; a mushroom body RNA binding protein; a myosin like proteins; a nemo-like kinase; a non-ATPase protein; a nuclear receptor NR1E1; a nucleic acid binding protein; a nucleoside diphosphate kinase (NBR-A); a oly(rC)-binding protein 2 (hnRNP-E1); a peroxisome biogenesis factor 1; a phosopholipid transporter involved in lipid metabolism; a phosphatase or enhancer of Pi uptake protein; a protease; a proteasome regulatory particle; a protein involved in cytoskeleton organization and/or biogenesis; a protein kinase associated with microtubules; a protein kinase mitogen-activated 7; a protein serine/threonine kinase involved in cell cycle, possibly targeted to cytoskeleton; a protein serine/threonine kinase involved in eye morphogenesis; a protein which associates with cdc25 phosphatase; a

protein which induces apoptosis; a ribonuclease P; a ribonuclease P protein subunit p29; a ser/thr phosphatase; a signal transduction protein; a signal transport protein; a sin3-associated polypeptide; a single stranded DNA/RNA binding protein; a sodium-dependent dicarboxylate transporters; a ssDNA/RNA binding proteins; a striatin, calmodulin-binding protein (STRN); a structural protein of ribosome involved in protein biosynthesis; a subtelomeric heterochromatin repeats; a sugar acetylase; a sugar modification protein; a suppresspr of ras; a tRNA processing enzyme Ribonuclease P protein subunit; a thyroid hormone responsive gene; a tie receptor protein tyrosine kinase; a transacylase; a transcription factor; a transcription factor involved in chromatin remodelling; a transcriptional regulation of c-myc expression; a transcriptional regulator; a transcriptional regulators/telomeric silencing; a translation initiation factor; a tumor metastasis inhibitor; a tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; a ubiquitin carrier protein; a ubiquitin-conjugating enzyme; a ugtUDP-glucose-glycoprotein glucosyltransferase; a zinc finger protein; an RNA polymerase II transcription factor; an acetylcholinesterase (YT blood group) precursor; an actin binding protein; an actin dependent regulator of chromatin; an acyl-CoA-binding protein; an alanine:glyoxylate aminotransferase; an alpha esterase; an ankyrin protein; an imitation-SWI protein; and an integrin beta 4 binding protein.

POLYPEPTIDES

It will be understood that polypeptides of the invention are not limited to polypeptides having the amino acid sequence set out in Examples 1 to 70 or fragments thereof but also include homologous sequences obtained from any source, for example related viral/bacterial proteins, cellular homologues and synthetic peptides, as well as variants or derivatives thereof.

Thus polypeptides of the invention also include those encoding homologues from other species including animals such as mammals (e.g. mice, rats or rabbits), especially primates, more especially humans. More specifically, homologues included within the scope of the invention include human homologues.

Thus, the present invention covers variants, homologues or derivatives of the amino acid sequence set out in Examples 1 to 70, as well as variants, homologues or derivatives of the nucleotide sequence coding for the amino acid sequences of the present invention.

In the context of the present invention, a homologous sequence is taken to include an amino acid sequence which is at least 15, 20, 25, 30, 40, 50, 60, 70, 80 or 90% identical, preferably at least 95 or 98% identical at the amino acid level over at least 50 or 100, preferably 200, 300, 400 or 500 amino acids with any one of the polypeptide sequences shown in the Examples. In particular, homology should typically be considered with respect to those regions of the sequence known to be essential for protein function rather than non-essential neighbouring sequences. This is especially important when considering homologous sequences from distantly related organisms.

Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These publicly and commercially available computer programs can calculate % homology between two or more sequences.

% homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues (for example less than 50 contiguous amino acids).

Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus

potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting "gaps" in the sequence alignment to try to maximise local homology.

However, these more complex methods assign "gap penalties" to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. "Affine gap costs" are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package (see below) the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A; Devereux *et al.,* 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel *et al.*, 1999 *ibid* – Chapter 18), FASTA (Atschul *et al.,* 1990, J. Mol. Biol., 403-410) and the GENEWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel *et al.*, 1999 *ibid*, pages 7-58 to 7-60). However it is preferred to use the GCG Bestfit program.

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each

pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for further details). It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

The terms "variant" or "derivative" in relation to the amino acid sequences of the present invention includes any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) amino acids from or to the sequence providing the resultant amino acid sequence retains substantially the same activity as the unmodified sequence, preferably having at least the same activity as the polypeptides presented in the sequence listings in the Examples.

Polypeptides having the amino acid sequence shown in the Examples, or fragments or homologues thereof may be modified for use in the present invention. Typically, modifications are made that maintain the biological activity of the sequence. Amino acid substitutions may be made, for example from 1, 2 or 3 to 10, 20 or 30 substitutions provided that the modified sequence retains the biological activity of the unmodified sequence. Alternatively, modifications may be made to deliberately inactivate one or more functional domains of the polypeptides of the invention. Amino acid substitutions may include the use of non-naturally occurring analogues, for example to increase blood plasma half-life of a therapeutically administered polypeptide.

Conservative substitutions may be made, for example according to the Table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

Polypeptides of the invention also include fragments of the full length sequences mentioned above. Preferably said fragments comprise at least one epitope. Methods of identifying epitopes are well known in the art. Fragments will typically comprise at least 6 amino acids, more preferably at least 10, 20, 30, 50 or 100 amino acids.

Proteins of the invention are typically made by recombinant means, for example as described below. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. Proteins of the invention may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis, GAL4 (DNA binding and/or transcriptional activation domains) and β-galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins of the invention may also be obtained by purification of cell extracts from animal cells.

Proteins of the invention may be in a substantially isolated form. It will be understood that the protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the protein and still be regarded as substantially isolated. A protein of the invention may also be in a substantially purified form, in which case it will generally comprise the protein in a preparation in which more than 90%, e.g. 95%, 98% or 99% of the protein in the preparation is a protein of the invention.

A polypeptide of the invention may be labeled with a revealing label. The revealing label may be any suitable label which allows the polypeptide to be detected. Suitable labels include radioisotopes, e.g. ^{125}I, enzymes, antibodies, polynucleotides and linkers such as biotin. Labeled polypeptides of the invention may be used in diagnostic procedures such as immunoassays to determine the amount of a polypeptide of the invention in a sample. Polypeptides or labeled polypeptides of the invention may also be used in serological or cell-mediated immune assays for the detection of immune reactivity to said polypeptides in animals and humans using standard protocols.

A polypeptide or labeled polypeptide of the invention or fragment thereof may also be fixed to a solid phase, for example the surface of an immunoassay well or dipstick. Such labeled and/or immobilised polypeptides may be packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like. Such polypeptides and kits may be used in methods of detection of antibodies to the polypeptides or their allelic or species variants by immunoassay.

Immunoassay methods are well known in the art and will generally comprise: (a) providing a polypeptide comprising an epitope bindable by an antibody against said protein; (b) incubating a biological sample with said polypeptide under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said polypeptide is formed.

Polypeptides of the invention may be used in *in vitro* or *in vivo* cell culture systems to study the role of their corresponding genes and homologues thereof in cell function, including their function in disease. For example, truncated or modified polypeptides may be introduced into a cell to disrupt the normal functions which occur in the cell. The polypeptides of the invention may be introduced into the cell by *in situ* expression of the polypeptide from a recombinant expression vector (see below). The expression vector optionally carries an inducible promoter to control the expression of the polypeptide.

The use of appropriate host cells, such as insect cells or mammalian cells, is expected to provide for such post-translational modifications (e.g. myristolation,

glycosylation, truncation, lapidation and tyrosine, serine or threonine phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention. Such cell culture systems in which polypeptides of the invention are expressed may be used in assay systems to identify candidate substances which interfere with or enhance the functions of the polypeptides of the invention in the cell.

POLYNUCLEOTIDES

Polynucleotides of the invention include polynucleotides that comprise any one or more of the nucleic acid sequences set out in Examples 1 to 70 and fragments thereof. Polynucleotides of the invention also include polynucleotides encoding the polypeptides of the invention. It will be understood by a skilled person that numerous different polynucleotides can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any particular host organism in which the polypeptides of the invention are to be expressed.

Polynucleotides of the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or life span of polynucleotides of the invention.

The terms “variant”, “homologue” or “derivative” in relation to the nucleotide sequence of the present invention include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the

sequence. Preferably said variant, homologues or derivatives code for a polypeptide having biological activity.

As indicated above, with respect to sequence homology, preferably there is at least 50 or 75%, more preferably at least 85%, more preferably at least 90% homology to the sequences shown in the sequence listing herein. More preferably there is at least 95%, more preferably at least 98%, homology. Nucleotide homology comparisons may be conducted as described above. A preferred sequence comparison program is the GCG Wisconsin Bestfit program described above. The default scoring matrix has a match value of 10 for each identical nucleotide and -9 for each mismatch. The default gap creation penalty is -50 and the default gap extension penalty is -3 for each nucleotide.

The present invention also encompasses nucleotide sequences that are capable of hybridising selectively to the sequences presented herein, or any variant, fragment or derivative thereof, or to the complement of any of the above. Nucleotide sequences are preferably at least 15 nucleotides in length, more preferably at least 20, 30, 40 or 50 nucleotides in length.

The term "hybridization" as used herein shall include "the process by which a strand of nucleic acid joins with a complementary strand through base pairing" as well as the process of amplification as carried out in polymerase chain reaction technologies.

Polynucleotides of the invention capable of selectively hybridising to the nucleotide sequences presented herein, or to their complement, will be generally at least 70%, preferably at least 80 or 90% and more preferably at least 95% or 98% homologous to the corresponding nucleotide sequences presented herein over a region of at least 20, preferably at least 25 or 30, for instance at least 40, 60 or 100 or more contiguous nucleotides.

The term "selectively hybridizable" means that the polynucleotide used as a probe is used under conditions where a target polynucleotide of the invention is found to hybridize to the probe at a level significantly above background. The background

hybridization may occur because of other polynucleotides present, for example, in the cDNA or genomic DNA library being screening. In this event, background implies a level of signal generated by interaction between the probe and a non-specific DNA member of the library which is less than 10 fold, preferably less than 100 fold as intense as the specific interaction observed with the target DNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with ^{32}P.

Hybridization conditions are based on the melting temperature (Tm) of the nucleic acid binding complex, as taught in Berger and Kimmel (1987, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol 152, Academic Press, San Diego CA), and confer a defined "stringency" as explained below.

Maximum stringency typically occurs at about Tm-5°C (5°C below the Tm of the probe); high stringency at about 5°C to 10°C below Tm; intermediate stringency at about 10°C to 20°C below Tm; and low stringency at about 20°C to 25°C below Tm. As will be understood by those of skill in the art, a maximum stringency hybridization can be used to identify or detect identical polynucleotide sequences while an intermediate (or low) stringency hybridization can be used to identify or detect similar or related polynucleotide sequences.

In a preferred aspect, the present invention covers nucleotide sequences that can hybridise to the nucleotide sequence of the present invention under stringent conditions (e.g. 65°C and 0.1xSSC {1xSSC = 0.15 M NaCl, 0.015 M Na_3 Citrate pH 7.0).

Where the polynucleotide of the invention is double-stranded, both strands of the duplex, either individually or in combination, are encompassed by the present invention. Where the polynucleotide is single-stranded, it is to be understood that the complementary sequence of that polynucleotide is also included within the scope of the present invention.

Polynucleotides which are not 100% homologous to the sequences of the present invention but fall within the scope of the invention can be obtained in a number of ways. Other variants of the sequences described herein may be obtained for example by probing

DNA libraries made from a range of individuals, for example individuals from different populations. In addition, other viral/bacterial, or cellular homologues particularly cellular homologues found in mammalian cells (e.g. rat, mouse, bovine and primate cells), may be obtained and such homologues and fragments thereof in general will be capable of selectively hybridising to the sequences shown in the Examples. Such sequences may be obtained by probing cDNA libraries made from or genomic DNA libraries from other animal species, and probing such libraries with probes comprising all or part of any on of the sequences shown in the Examples under conditions of medium to high stringency. The nucleotide sequences of the human homologues described in the Examples, may preferably be used to identify other primate/mammalian homologues since nucleotide homology between human sequences and mammalian sequences is likely to be higher than is the case for the *Drosophila* sequences identified herein.

Similar considerations apply to obtaining species homologues and allelic variants of the polypeptide or nucleotide sequences of the invention.

Variants and strain/species homologues may also be obtained using degenerate PCR which will use primers designed to target sequences within the variants and homologues encoding conserved amino acid sequences within the sequences of the present invention. Conserved sequences can be predicted, for example, by aligning the amino acid sequences from several variants/homologues. Sequence alignments can be performed using computer software known in the art. For example the GCG Wisconsin PileUp program is widely used.

The primers used in degenerate PCR will contain one or more degenerate positions and will be used at stringency conditions lower than those used for cloning sequences with single sequence primers against known sequences. It will be appreciated by the skilled person that overall nucleotide homology between sequences from distantly related organisms is likely to be very low and thus in these situations degenerate PCR may be the method of choice rather than screening libraries with labeled fragments the sequences disclosed in the Examples.

In addition, homologous sequences may be identified by searching nucleotide and/or protein databases using search algorithms such as the BLAST suite of programs. This approach is described in the Examples.

Alternatively, such polynucleotides may be obtained by site directed mutagenesis of characterised sequences, such as the sequences disclosed in the Examples. This may be useful where for example silent codon changes are required to sequences to optimise codon preferences for a particular host cell in which the polynucleotide sequences are being expressed. Other sequence changes may be desired in order to introduce restriction enzyme recognition sites, or to alter the property or function of the polypeptides encoded by the polynucleotides. For example, further changes may be desirable to represent particular coding changes found in the sequences disclosed in the Examples which give rise to mutant genes which have lost their regulatory function. Probes based on such changes can be used as diagnostic probes to detect such mutants.

Polynucleotides of the invention may be used to produce a primer, e.g. a PCR primer, a primer for an alternative amplification reaction, a probe e.g. labeled with a revealing label by conventional means using radioactive or non-radioactive labels, or the polynucleotides may be cloned into vectors. Such primers, probes and other fragments will be at least 8, 9, 10, or 15, preferably at least 20, for example at least 25, 30 or 40 nucleotides in length, and are also encompassed by the term polynucleotides of the invention as used herein.

Polynucleotides such as a DNA polynucleotides and probes according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques.

In general, primers will be produced by synthetic means, involving a step wise manufacture of the desired nucleic acid sequence one nucleotide at a time. Techniques for accomplishing this using automated techniques are readily available in the art.

Longer polynucleotides will generally be produced using recombinant means, for example using a PCR (polymerase chain reaction) cloning techniques. This will involve making a pair of primers (e.g. of about 15 to 30 nucleotides) flanking a region of the lipid targeting sequence which it is desired to clone, bringing the primers into contact with mRNA or cDNA obtained from an animal or human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction mixture on an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a suitable cloning vector

Polynucleotides or primers of the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{35}S, enzyme labels, or other protein labels such as biotin. Such labels may be added to polynucleotides or primers of the invention and may be detected using by techniques known *per se*.

Polynucleotides or primers of the invention or fragments thereof labeled or unlabeled may be used by a person skilled in the art in nucleic acid-based tests for detecting or sequencing polynucleotides of the invention in the human or animal body.

Such tests for detecting generally comprise bringing a biological sample containing DNA or RNA into contact with a probe comprising a polynucleotide or primer of the invention under hybridising conditions and detecting any duplex formed between the probe and nucleic acid in the sample. Such detection may be achieved using techniques such as PCR or by immobilising the probe on a solid support, removing nucleic acid in the sample which is not hybridised to the probe, and then detecting nucleic acid which has hybridised to the probe. Alternatively, the sample nucleic acid may be immobilised on a solid support, and the amount of probe bound to such a support can be detected. Suitable assay methods of this and other formats can be found in for example WO89/03891 and WO90/13667.

Tests for sequencing nucleotides of the invention include bringing a biological sample containing target DNA or RNA into contact with a probe comprising a polynucleotide or primer of the invention under hybridising conditions and determining the sequence by, for example the Sanger dideoxy chain termination method (see Sambrook *et al.*).

Such a method generally comprises elongating, in the presence of suitable reagents, the primer by synthesis of a strand complementary to the target DNA or RNA and selectively terminating the elongation reaction at one or more of an A, C, G or T/U residue; allowing strand elongation and termination reaction to occur; separating out according to size the elongated products to determine the sequence of the nucleotides at which selective termination has occurred. Suitable reagents include a DNA polymerase enzyme, the deoxynucleotides dATP, dCTP, dGTP and dTTP, a buffer and ATP. Dideoxynucleotides are used for selective termination.

Tests for detecting or sequencing nucleotides of the invention in a biological sample may be used to determine particular sequences within cells in individuals who have, or are suspected to have, an altered gene sequence, for example within cancer cells including leukaemia cells and solid tumours such as breast, ovary, lung, colon, pancreas, testes, liver, brain, muscle and bone tumours. Cells from patients suffering from a proliferative disease may also be tested in the same way.

In addition, the identification of the genes described in the Examples will allow the role of these genes in hereditary diseases to be investigated. In general, this will involve establishing the status of the gene (e.g. using PCR sequence analysis), in cells derived from animals or humans with, for example, neurological disorders or neoplasms.

The probes of the invention may conveniently be packaged in the form of a test kit in a suitable container. In such kits the probe may be bound to a solid support where the assay format for which the kit is designed requires such binding. The kit may also contain suitable reagents for treating the sample to be probed, hybridising the probe to nucleic acid in the sample, control reagents, instructions, and the like.

NUCLEIC ACID VECTORS

Polynucleotides of the invention can be incorporated into a recombinant replicable vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells include bacteria such as *E. coli*, yeast, mammalian cell lines and other eukaryotic cell lines, for example insect Sf9 cells.

Preferably, a polynucleotide of the invention in a vector is operably linked to a control sequence that is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector. The term "operably linked" means that the components described are in a relationship permitting them to function in their intended manner. A regulatory sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences.

The control sequences may be modified, for example by the addition of further transcriptional regulatory elements to make the level of transcription directed by the control sequences more responsive to transcriptional modulators.

Vectors of the invention may be transformed or transfected into a suitable host cell as described below to provide for expression of a protein of the invention. This process may comprise culturing a host cell transformed with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the protein, and optionally recovering the expressed protein. Vectors will be chosen that are compatible with the host cell used.

The vectors may be for example, plasmid or virus vectors provided with an origin of replication, optionally a promoter for the expression of the said polynucleotide and

optionally a regulator of the promoter. The vectors may contain one or more selectable marker genes, for example an ampicillin resistance gene in the case of a bacterial plasmid or a neomycin resistance gene for a mammalian vector. Vectors may be used, for example, to transfect or transform a host cell.

Control sequences operably linked to sequences encoding the polypeptide of the invention include promoters/enhancers and other expression regulation signals. These control sequences may be selected to be compatible with the host cell for which the expression vector is designed to be used in. The term promoter is well-known in the art and encompasses nucleic acid regions ranging in size and complexity from minimal promoters to promoters including upstream elements and enhancers.

The promoter is typically selected from promoters which are functional in mammalian cells, although prokaryotic promoters and promoters functional in other eukaryotic cells, such as insect cells, may be used. The promoter is typically derived from promoter sequences of viral or eukaryotic genes. For example, it may be a promoter derived from the genome of a cell in which expression is to occur. With respect to eukaryotic promoters, they may be promoters that function in a ubiquitous manner (such as promoters of α-actin, β-actin, tubulin) or, alternatively, a tissue-specific manner (such as promoters of the genes for pyruvate kinase). They may also be promoters that respond to specific stimuli, for example promoters that bind steroid hormone receptors. Viral promoters may also be used, for example the Moloney murine leukaemia virus long terminal repeat (MMLV LTR) promoter, the rous sarcoma virus (RSV) LTR promoter or the human cytomegalovirus (CMV) IE promoter.

It may also be advantageous for the promoters to be inducible so that the levels of expression of the heterologous gene can be regulated during the life-time of the cell. Inducible means that the levels of expression obtained using the promoter can be regulated.

In addition, any of these promoters may be modified by the addition of further regulatory sequences, for example enhancer sequences. Chimeric promoters may also be

used comprising sequence elements from two or more different promoters described above.

Polynucleotides according to the invention may also be inserted into the vectors described above in an antisense orientation to provide for the production of antisense RNA. Antisense RNA or other antisense polynucleotides may also be produced by synthetic means. Such antisense polynucleotides may be used in a method of controlling the levels of RNAs transcribed from genes comprising any one of the polynucleotides of the invention.

HOST CELLS

Vectors and polynucleotides of the invention may be introduced into host cells for the purpose of replicating the vectors/polynucleotides and/or expressing the polypeptides of the invention encoded by the polynucleotides of the invention. Although the polypeptides of the invention may be produced using prokaryotic cells as host cells, it is preferred to use eukaryotic cells, for example yeast, insect or mammalian cells, in particular mammalian cells.

Vectors/polynucleotides of the invention may be introduced into suitable host cells using a variety of techniques known in the art, such as transfection, transformation and electroporation. Where vectors/polynucleotides of the invention are to be administered to animals, several techniques are known in the art, for example infection with recombinant viral vectors such as retroviruses, herpes simplex viruses and adenoviruses, direct injection of nucleic acids and biolistic transformation.

PROTEIN EXPRESSION AND PURIFICATION

Host cells comprising polynucleotides of the invention may be used to express polypeptides of the invention. Host cells may be cultured under suitable conditions which allow expression of the proteins of the invention. Expression of the polypeptides of the invention may be constitutive such that they are continually produced, or inducible, requiring a stimulus to initiate expression. In the case of inducible expression, protein

production can be initiated when required by, for example, addition of an inducer substance to the culture medium, for example dexamethasone or IPTG.

Polypeptides of the invention can be extracted from host cells by a variety of techniques known in the art, including enzymatic, chemical and/or osmotic lysis and physical disruption.

Polypeptides of the invention may also be produced recombinantly in an *in vitro* cell-free system, such as the TnT™ (Promega) rabbit reticulocyte system.

ANTIBODIES

The invention also provides monoclonal or polyclonal antibodies to polypeptides of the invention or fragments thereof. Thus, the present invention further provides a process for the production of monoclonal or polyclonal antibodies to polypeptides of the invention.

If polyclonal antibodies are desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunised with an immunogenic polypeptide bearing an epitope(s) from a polypeptide of the invention. Serum from the immunised animal is collected and treated according to known procedures. If serum containing polyclonal antibodies to an epitope from a polypeptide of the invention contains antibodies to other antigens, the polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art. In order that such antibodies may be made, the invention also provides polypeptides of the invention or fragments thereof haptenised to another polypeptide for use as immunogens in animals or humans.

Monoclonal antibodies directed against epitopes in the polypeptides of the invention can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. Panels of monoclonal antibodies produced against epitopes in the

polypeptides of the invention can be screened for various properties; i.e., for isotype and epitope affinity.

An alternative technique involves screening phage display libraries where, for example the phage express scFv fragments on the surface of their coat with a large variety of complementarity determining regions (CDRs). This technique is well known in the art.

Antibodies, both monoclonal and polyclonal, which are directed against epitopes from polypeptides of the invention are particularly useful in diagnosis, and those which are neutralising are useful in passive immunotherapy. Monoclonal antibodies, in particular, may be used to raise anti-idiotype antibodies. Anti-idiotype antibodies are immunoglobulins which carry an "internal image" of the antigen of the agent against which protection is desired.

Techniques for raising anti-idiotype antibodies are known in the art. These anti-idiotype antibodies may also be useful in therapy.

For the purposes of this invention, the term "antibody", unless specified to the contrary, includes fragments of whole antibodies which retain their binding activity for a target antigen. Such fragments include Fv, F(ab') and $F(ab')_2$ fragments, as well as single chain antibodies (scFv). Furthermore, the antibodies and fragments thereof may be humanised antibodies, for example as described in EP-A-239400.

Antibodies may be used in method of detecting polypeptides of the invention present in biological samples by a method which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

Suitable samples include extracts tissues such as brain, breast, ovary, lung, colon, pancreas, testes, liver, muscle and bone tissues or from neoplastic growths derived from such tissues.

Antibodies of the invention may be bound to a solid support and/or packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like.

Assays

The present invention provides assays that are suitable for identifying substances which bind to polypeptides of the invention and which affect, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, cytokinesis functions, chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation, microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In addition, assays suitable for identifying substances that interfere with binding of polypeptides of the invention, where appropriate, to components of cell division cycle machinery. This includes not only components such as microtubules but also signalling components and regulatory components as indicated above. Such assays are typically *in vitro*. Assays are also provided that test the effects of candidate substances identified in preliminary *in vitro* assays on intact cells in whole cell assays. The assays described below, or any suitable assay as known in the art, may be used to identify these substances.

According to one aspect of the invention, therefore, we provide one or more substances identified by any of the assays described below, *viz*, mitosis assays, meiotic assays, polypeptide binding assays, microtubule binding/polymerisation assays, microtubule purification and binding assays, microtubule organising centre (MTOC) nucleation activity assays, motor protein assay, assay for spindle assembly and function,

assays for dna replication, chromosome condensation assays, kinase assays, kinase inhibitor assays, and whole cell assays, each as described in further detail below.

CANDIDATE SUBSTANCES

A substance that inhibits cell cycle progression as a result of an interaction with a polypeptide of the invention may do so in several ways. For example, if the substance inhibits cell division, mitosis and/or meiosis, it may directly disrupt the binding of a polypeptide of the invention to a component of the spindle apparatus by, for example, binding to the polypeptide and masking or altering the site of interaction with the other component. A substance which inhibits DNA replication may do so by inhibiting the phosphorylation or de-phosphorylation of proteins involved in replication. For example, it is known that the kinase inhibitor 6-DMAP (6-dimethylaminopurine) prevents the initiation of replication (Blow, JJ, 1993, *J Cell Biol*122,993-1002). Candidate substances of this type may conveniently be preliminarily screened by *in vitro* binding assays as, for example, described below and then tested, for example in a whole cell assay as described below. Examples of candidate substances include antibodies which recognise a polypeptide of the invention.

A substance which can bind directly to a polypeptide of the invention may also inhibit its function in cell cycle progression by altering its subcellular localisation and hence its ability to interact with its normal substrate. The substance may alter the subcellular localisation of the polypeptide by directly binding to it, or by indirectly disrupting the interaction of the polypeptide with another component. For example, it is known that interaction between the p68 and p180 subunits of DNA polymerase alpha-primase enzyme is necessary in order for p180 to translocate into the nucleus (Mizuno et al (1998) *Mol Cell Biol*18,3552-62), and accordingly, a substance which disrupts the interaction between p68 and p180 will affect nuclear translocation and hence activity of the primase. A substance which affects mitosis may do so by preventing the polypeptide and components of the mitotic apparatus from coming into contact within the cell.
These substances may be tested using, for example the whole cells assays described below. Non-functional homologues of a polypeptide of the invention may also be tested

for inhibition of cell cycle progression since they may compete with the wild type protein for binding to components of the cell division cycle machinery whilst being incapable of the normal functions of the protein or block the function of the protein bound to the cell division cycle machinery. Such non-functional homologues may include naturally occurring mutants and modified sequences or fragments thereof.

Alternatively, instead of preventing the association of the components directly, the substance may suppress the biologically available amount of a polypeptide of the invention. This may be by inhibiting expression of the component, for example at the level of transcription, transcript stability, translation or post-translational stability. An example of such a substance would be antisense RNA or double-stranded interfering RNA sequences which suppresses the amount of mRNA biosynthesis.

Suitable candidate substances include peptides, especially of from about 5 to 30 or 10 to 25 amino acids in size, based on the sequence of the polypeptides described in the Examples, or variants of such peptides in which one or more residues have been substituted. Peptides from panels of peptides comprising random sequences or sequences which have been varied consistently to provide a maximally diverse panel of peptides may be used.

Suitable candidate substances also include antibody products (for example, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies and CDR-grafted antibodies) which are specific for a polypeptide of the invention. Furthermore, combinatorial libraries, peptide and peptide mimetics, defined chemical entities, oligonucleotides, and natural product libraries may be screened for activity as inhibitors of binding of a polypeptide of the invention to the cell division cycle machinery, for example mitotic/meiotic apparatus (such as microtubules). The candidate substances may be used in an initial screen in batches of, for example 10 substances per reaction, and the substances of those batches which show inhibition tested individually. Candidate substances which show activity in *in vitro* screens such as those described below can then be tested in whole cell systems, such as mammalian cells which will be exposed to the inhibitor and tested for inhibition of any of the stages of the cell cycle.

Polypeptide Binding Assays

One type of assay for identifying substances that bind to a polypeptide of the invention involves contacting a polypeptide of the invention, which is immobilised on a solid support, with a non-immobilised candidate substance determining whether and/or to what extent the polypeptide of the invention and candidate substance bind to each other. Alternatively, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

In a preferred assay method, the polypeptide of the invention is immobilised on beads such as agarose beads. Typically this is achieved by expressing the component as a GST-fusion protein in bacteria, yeast or higher eukaryotic cell lines and purifying the GST-fusion protein from crude cell extracts using glutathione-agarose beads (Smith and Johnson, 1988). As a control, binding of the candidate substance, which is not a GST-fusion protein, to the immobilised polypeptide of the invention is determined in the absence of the polypeptide of the invention. The binding of the candidate substance to the immobilised polypeptide of the invention is then determined. This type of assay is known in the art as a GST pulldown assay. Again, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

It is also possible to perform this type of assay using different affinity purification systems for immobilising one of the components, for example Ni-NTA agarose and histidine-tagged components.

Binding of the polypeptide of the invention to the candidate substance may be determined by a variety of methods well-known in the art. For example, the non-immobilised component may be labeled (with for example, a radioactive label, an epitope tag or an enzyme-antibody conjugate). Alternatively, binding may be determined by immunological detection techniques. For example, the reaction mixture can be Western blotted and the blot probed with an antibody that detects the non-immobilised component. ELISA techniques may also be used.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final concentration used is typically from 100 to 500 μg/ml, more preferably from 200 to 300 μg/ml.

Microtubule Binding/Polymerisation Assays

In the case of polypeptides of the invention that bind to microtubules, another type of *in vitro* assay involves determining whether a candidate substance modulates binding of a polypeptide of the invention to microtubules . Such an assay typically comprises contacting a polypeptide of the invention with microtubules in the presence or absence of the candidate substance and determining if the candidate substance has an affect on the binding of the polypeptide of the invention to the microtubules. This assay can also be used in the absence of candidate substances to confirm that a polypeptide of the invention does indeed bind to microtubules. Microtubules may be prepared and assays conducted as follows:

Microtubule Purification and Binding Assays

Microtubules are purified from 0-3h-old *Drosophila* embryos essentially as described previously (Saunders, *et al.*, 1997). About 3 ml of embryos are homogenized with a Dounce homogenizer in 2 volumes of ice-cold lysis buffer (0.1 M Pipes/NaOH, pH6.6, 5 mM EGTA, 1 mM MgSO4, 0.9 M glycerol, 1 mM DTT, 1 mM PMSF, 1 μg/ml aprotinin, 1 μg/ml leupeptin and 1 μg/ml pepstatin). The microtubules are depolymerized by incubation on ice for 15 min, and the extract is then centrifuged at 16,000 g for 30 min at 4°C. The supernatant is recentrifuged at 135,000 g for 90 min at 4°C. Microtubules in this later supernatant are polymerized by addition of GTP to 1 mM and taxol to 20 μM and incubation at room temperature for 30 min. A 3 ml aliquot of the extract is layered on top of 3 ml 15% sucrose cushion prepared in lysis buffer. After centrifuging at 54,000g for 30 min at 20°C using a swing out rotor, the microtubule pellet is resuspended in lysis buffer.

Microtubule overlay assays are performed as previously described (Saunders *et al.*, 1997). 500 ng per lane of recombinant Asp, recombinant polypeptide, and bovine serum albumin (BSA, Sigma) are fractionated by 10% SDS-PAGE and blotted onto PVDF

membranes (Millipore). The membranes are preincubated in TBST (50mM Tris pH 7.5, 150 mM NaCl, 0.05% Tween 20) containing 5% low fat powdered milk (LFPM) for 1 h and then washed 3 times for 15 min in lysis buffer. The filters are then incubated for 30 minutes in lysis buffer containing either 1 mM GDP, 1 mM GTP, or 1 mM GTP-γ-S. MAP-free bovine brain tubulin (Molecular Probes) is polymerised at a concentration of 2 μg/ml in lysis buffer by addition of GTP to a final concentration of 1 mM and incubated at 37°C for 30 min. The nucleotide solutions are removed and the buffer containing polymerised microtubules added to the membanes for incubation for 1h at 37°C with addition of taxol at a final concentration of 10 μM for the final 30 min. The blots are then washed 3 times with TBST and the bound tubulin detected using standard Western blot procedures using anti-β-tubulin antibodies (Boehringer Manheim) at 2.5 μg/ml and the Super Signal detection system (Pierce).

It may be desirable in one embodiment of this type of assay to deplete the polypeptide of the invention from cell extracts used to produce polymerise microtubules. This may, for example, be achieved by the use of suitable antibodies.

A simple extension to this type of assay would be to test the effects of purified polypeptide of the invention upon the ability of tubulin to polymerise *in vitro* (for example, as used by Andersen and Karsenti, 1997) in the presence or absence of a candidate substance (typically added at the concentrations described above). *Xenopus* cell-free extracts may conveniently be used, for example as a source of tubulin.

Microtubule Organising Centre (MTOC) Nucleation Activity Assays

Candidate substances, for example those identified using the binding assays described above, may be screening using a microtubule organising centre nucleation activity assay to determine if they are capable of disrupting MTOCs as measured by, for example, aster formation. This assay in its simplest form comprises adding the candidate substance to a cellular extract which in the absence of the candidate substance has microtubule organising centre nucleation activity resulting in formation of asters.

In a preferred embodiment, the assay system comprises (i) a polypeptide of the invention and (ii) components required for microtubule organising centre nucleation activity except for functional polypeptide of the invention, which is typically removed by immunodepletion (or by the use of extracts from mutant cells). The components themselves are typically in two parts such that microtubule nucleation does not occur until the two parts are mixed. The polypeptide of the invention may be present in one of the two parts initially or added subsequently prior to mixing of the two parts.

Subsequently, the polypeptide of the invention and candidate substance are added to the component mix and microtubule nucleation from centrosomes measured, for example by immunostaining for the polypeptide of the invention and visualising aster formation by immuno-fluorescence microscopy. The polypeptide of the invention may be preincubated with the candidate substance before addition to the component mix. Alternatively, both the polypeptide of the invention and the candidate substance may be added directly to the component mix, simultaneously or sequentially in either order.

The components required for microtubule organising centre formation typically include salt-stripped centrosomes prepared as described in Moritz *et al.*, 1998. Stripping centrosome preparations with 2 M KI removes the centrosome proteins CP60, CP190, CNN and γ-tubulin. Of these, neither CP60 nor CP190 appear to be required for microtubule nucleation. The other minimal components are typically provided as a depleted cellular extract, or conveniently, as a cellular extract from cells with a non-functional variant of a polypeptide of the invention. Typically, labeled tubulin (usually β-tubulin) is also added to assist in visualising aster formation.

Alternatively, partially purified centrosomes that have not been salt-stripped may be used as part of the components. In this case, only tubulin, preferably labeled tubulin is required to complete the component mix.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final

concentration used is typically from 100 to 500 μg/ml, more preferably from 200 to 300 μg/ml.

The degree of inhibition of aster formation by the candidate substance may be determined by measuring the number of normal asters per unit area for control untreated cell preparation and measuring the number of normal asters per unit area for cells treated with the candidate substance and comparing the result. Typically, a candidate substance is considered to be capable of disrupting MTOC integrity if the treated cell preparations have less than 50%, preferably less than 40, 30, 20 or 10% of the number of asters found in untreated cells preparations. It may also be desirable to stain cells for γ-tubulin to determine the maximum number of possible MTOCs present to allow normalisation between samples.

Motor Protein Assay

Polypeptides of the invention may interact with motor proteins such as the Eg5-like motor protein *in vitro*. The effects of candidate substances on such a process may be determined using assays wherein the motor protein is immobilised on coverslips. Rhodamine labeled microtubules are then added and their translocation can be followed by fluorescent microscopy. The effect of candidate substances may thus be determined by comparing the extent and/or rate of translocation in the presence and absence of the candidate substance. Generally, candidate substances known to bind to a polypeptide of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of motor proteins and the resulting identified substances tested for affects on a polypeptide of the invention as described above.

Typically this assay uses microtubules stabilised by taxol (e.g. Howard and Hyman 1993; Chandra and Endow, 1993 – both chapters in "Motility Assays for Motor Proteins" Ed Jon Scholey, pub Academic Press). If however, a polypeptide of the invention were to promote stable polymerisation of microtubules (see above) then these microtubules could be used directly in motility assays.

Simple protein-protein binding assays as described above, using a motor protein and a polypeptide of the invention may also be used to confirm that the polypeptide of the invention binds to the motor protein, typically prior to testing the effect of candidate substances on that interaction.

Assay for Spindle Assembly and Function

A further assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is an assay which measures spindle assembly and function. Typically, such assays are performed using *Xenopus* cell free systems, where two types of spindle assembly are possible. In the "half spindle" assembly pathway, a cytoplasmic extract of CSF arrested oocytes is mixed with sperm chromatin. The half spindles that form subsequently fuse together. A more physiological method is to induce CSF arrested extracts to enter interphase by addition of calcium, whereupon the DNA replicates and kinetochores form. Addition of fresh CSF arrested extract then induces mitosis with centrosome duplication and spindle formation (for discussion of these systems see Tournebize and Heald, 1996).

Again, generally, candidate substances known to bind to a polypeptide of the invention, or non-functional polypeptide variants of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of spindle formation and function and the resulting identified substances tested for affects binding of the polypeptide of the invention as described above.

Assays for DNA Replication

Another assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is as assay for replication of DNA. A number of cell free systems have been developed to assay DNA replication. These can be used to assay the ability of a substance to prevent or inhibit DNA replication, by conducting the assay in the presence of the substance. Suitable cell-free assay systems include, for example the SV-40 assay (Li and Kelly, 1984, *Proc. Natl. Acad. Sci USA* 81, 6973-6977; Waga and Stillman, 1994, *Nature* 369, 207-212.). A *Drosophila* cell free replication system, for example as described by Crevel and Cotteril (1991), *EMBO J.* 10,

4361-4369, may also be used. A preferred assay is a cell free assay derived from *Xenopus* egg low speed supernatant extracts described in Blow and Laskey (1986, *Cell* 47,577-587) and Sheehan et al. (1988, *J. Cell Biol.* 106, 1-12), which measures the incorporation of nucleotides into a substrate consisting of *Xenopus* sperm DNA or HeLa nuclei. The nucleotides may be radiolabelled and incorporation assayed by scintillation counting. Alternatively and preferably, bromo-deoxy-uridine (BrdU) is used as a nucleotide substitute and replication activity measured by density substitution. The latter assay is able to distinguish genuine replication initiation events from incorporation as a result of DNA repair. The human cell-free replication assay reported by Krude, et al (1997), *Cell* 88, 109-19 may also be used to assay the effects of substances on the polypeptides of the invention.

Other* In Vitro *Assays

Other assays for identifying substances that bind to a polypeptide of the invention are also provided. For example, substances which affect chromosome condensation may be assayed using the *in vitro* cell free system derived from *Xenopus* eggs, as known in the art.

Substances which affect kinase activity or proteolysis activity are of interest. It is known, for example, that temporal control of ubiquitin-proteasome mediated protein degradation is critical for normal G1 and S phase progression (reviewed in Krek 1998, *Curr Opin Genet Dev* 8, 36-42). A number of E3 ubiquitin protein ligases, designated SCFs (Skp1-cullin-F-box protein ligase complexes), confer substrate specificity on ubiquitination reactions, while protein kinases phosphorylate substrates destined for destruction and convert them into preferred targets for ubiquitin modification catalyzed by SCFs. Furthermore, ubiquitin-mediated proteolysis due to the anaphase-promoting complex/cyclosome (APC/C) is essential for separation of sister chromatids during mitosis, and exit from mitosis (Listovsky et al., 2000, *Exp Cell Res* 255, 184-191).

Substances which inhibit or affect kinase activity may be identified by means of a kinase assay as known in the art, for example, by measuring incorporation of ^{32}P into a suitable peptide or other substrate in the presence of the candidate substance. Similarly,

substances which inhibit or affect proteolytic activity may be assayed by detecting increased or decreased cleavage of suitable polypeptide substrates.

Assays for these and other protein or polypeptide activities are known to those skilled in the art, and may suitably be used to identify substances which bind to a polypeptide of the invention and affect its activity.

Whole Cell Assays

Candidate substances may also be tested on whole cells for their effect on cell cycle progression, including mitosis and/or meiosis. Preferably the candidate substances have been identified by the above-described *in vitro* methods. Alternatively, rapid throughput screens for substances capable of inhibiting cell division, typically mitosis, may be used as a preliminary screen and then used in the *in vitro* assay described above to confirm that the affect is on a particular polypeptide of the invention.

The candidate substance, i.e. the test compound, may be administered to the cell in several ways. For example, it may be added directly to the cell culture medium or injected into the cell. Alternatively, in the case of polypeptide candidate substances, the cell may be transfected with a nucleic acid construct which directs expression of the polypeptide in the cell. Preferably, the expression of the polypeptide is under the control of a regulatable promoter.

Typically, an assay to determine the effect of a candidate substance identified by the method of the invention on a particular stage of the cell division cycle comprises administering the candidate substance to a cell and determining whether the substance inhibits that stage of the cell division cycle. Techniques for measuring progress through the cell cycle in a cell population are well known in the art. The extent of progress through the cell cycle in treated cells is compared with the extent of progress through the cell cycle in an untreated control cell population to determine the degree of inhibition, if any. For example, an inhibitor of mitosis or meiosis may be assayed by measuring the proportion of cells in a population which are unable to undergo mitosis/meiosis and comparing this to the proportion of cells in an untreated population.

The concentration of candidate substances used will typically be such that the final concentration in the cells is similar to that described above for the *in vitro* assays.

A candidate substance is typically considered to be an inhibitor of a particular stage in the cell division cycle (for example, mitosis) if the proportion of cells undergoing that particular stage (i.e., mitosis) is reduced to below 50%, preferably below 40, 30, 20 or 10% of that observed in untreated control cell populations.

THERAPEUTIC USES

Many tumours are associated with defects in cell cycle progression, for example loss of normal cell cycle control. Tumour cells may therefore exhibit rapid and often aberrant mitosis. One therapeutic approach to treating cancer may therefore be to inhibit mitosis in rapidly dividing cells. Such an approach may also be used for therapy of any proliferative disease in general. Thus, since the polypeptides of the invention appear to be required for normal cell cycle progression, they represent targets for inhibition of their functions, particularly in tumour cells and other proliferative cells.

The term proliferative disorder is used herein in a broad sense to include any disorder that requires control of the cell cycle, for example, cardiovascular disorders such as restenosis and cardiomyopathy, auto-immune disorders such as glomerulonephritis and rheumatoid arthritis, dermatological disorders such as psoriasis, anti-inflammatory, anti-fungal, antiparasitic disorders such as malaria, emphysema and alopecia.

One possible approach is to express anti-sense constructs directed against polynucleotides of the invention, preferably selectively in tumour cells, to inhibit gene function and prevent the tumour cell from progressing through the cell cycle. Anti-sense constructs may also be used to inhibit gene function to prevent cell cycle progression in a proliferative cell. Another approach is to use non-functional variants of polypeptides of the invention that compete with the endogenous gene product for cellular components of cell cycle machinery, resulting in inhibition of function. Alternatively, compounds identified by the assays described above as binding to a polypeptide of the invention may

be administered to tumour or proliferative cells to prevent the function of that polypeptide. This may be performed, for example, by means of gene therapy or by direct administration of the compounds. Suitable antibodies of the invention may also be used as therapeutic agents.

Alternatively, double-stranded (ds) RNA is a powerful way of interfering with gene expression in a range of organisms that has recently been shown to be successful in mammals (Wianny and Zernicka-Goetz, 2000, Nat Cell Biol 2000, 2, 70-75). Double stranded RNA corresponding to the sequence of a polynucleotide according to the invention can be introduced into or expressed in oocytes and cells of a candidate organism to interfere with cell division cycle progression.

In addition, a number of the mutations described herein exhibit aberrant meiotic phenotypes. Aberrant meiosis is an important factor in infertility since mutations that affect only meiosis and not mitosis will lead to a viable organism but one that is unable to produce viable gametes and hence reproduce. Consequently, the elucidation of genes involved in meiosis is an important step in diagnosing and preventing/treating fertility problems. Thus the polypeptides of the invention identified in mutant *Drosophila* having meiotic defects (as is clearly indicated in the Examples) may be used in methods of identifying substances that affect meiosis. In addition, these polypeptides, and corresponding polynucleotides, may be used to study meiosis and identify possible mutations that are indicative of infertility. This will be of use in diagnosing infertility problems.

ADMINISTRATION

Substances identified or identifiable by the assay methods of the invention may preferably be combined with various components to produce compositions of the invention. Preferably the compositions are combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition (which may be for human or animal use). Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition of the invention may be administered by

direct injection. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration. Typically, each protein may be administered at a dose of from 0.01 to 30 mg/kg body weight, preferably from 0.1 to 10 mg/kg, more preferably from 0.1 to 1 mg/kg body weight.

Polynucleotides/vectors encoding polypeptide components (or antisense constructs) for use in inhibiting cell cycle progression, for example, inhibiting mitosis or meiosis, may be administered directly as a naked nucleic acid construct. They may further comprise flanking sequences homologous to the host cell genome. When the polynucleotides/vectors are administered as a naked nucleic acid, the amount of nucleic acid administered may typically be in the range of from 1 μg to 10 mg, preferably from 100 μg to 1 mg. It is particularly preferred to use polynucleotides/ vectors that target specifically tumour or proliferative cells, for example by virtue of suitable regulatory constructs or by the use of targeted viral vectors.

Uptake of naked nucleic acid constructs by mammalian cells is enhanced by several known transfection techniques for example those including the use of transfection agents. Example of these agents include cationic agents (for example calcium phosphate and DEAE-dextran) and lipofectants (for example lipofectam™ and transfectam™). Typically, nucleic acid constructs are mixed with the transfection agent to produce a composition.

Preferably the polynucleotide, polypeptide, compound or vector described here may be conjugated, joined, linked, fused, or otherwise associated with a membrane translocation sequence.

Preferably, the polynucleotide, polypeptide, compound or vector, etc described here may be delivered into cells by being conjugated with, joined to, linked to, fused to, or otherwise associated with a protein capable of crossing the plasma membrane and/or the nuclear membrane (i.e., a membrane translocation sequence). Preferably, the substance of interest is fused or conjugated to a domain or sequence from such a protein responsible for the translocational activity. Translocation domains and sequences for example include

domains and sequences from the HIV-1-trans-activating protein (Tat), *Drosophila* Antennapedia homeodomain protein and the herpes simplex-1 virus VP22 protein. In a highly preferred embodiment, the substance of interest is conjugated with penetratin protein or a fragment of this. Penetratin comprises the sequence RQIKIWFQNRRMKWKK and is described in Derossi, *et al.*, (1994), *J. Biol. Chem.* 269, 10444-50; use of penetratin-drug conjugates for intracellular delivery is described in WO/00/01417. Truncated and modified forms of penetratin may also be used, as described in WO/00/29427.

Preferably the polynucleotide, polypeptide, compound or vector according to the invention is combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition. Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration.

The routes of administration and dosages described are intended only as a guide since a skilled practitioner will be able to determine readily the optimum route of administration and dosage for any particular patient and condition.

The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not intended in any way to limit the scope of the invention.

EXAMPLES

Generation and Identification of Lethal, Semi-Lethal and Sterile Third Chromosome Mutants Having Defects in Mitosis and/Or Meiosis, and Second Chromosome Mutants Having Defects in Imaginal Disc Development By P-Element Insertion Mutagenesis

P-element mutagenesis

Transposable elements are widely used for mutagenesis in *Drosophila melanogaster* as they couple the advantages of providing effective genetic lesions with ease of detecting disrupted genes for the purpose of molecular cloning. To achieve near saturation of the genome with mutations resulting from mobilisation of the P-lacW transposon (a P-element marked with a mini-white gene, bearing the *E.coli lacZ* gene as an enhancer trap, and an *E.coli* replicon and ampicillin resistance gene to facilitate 'plasmid rescue' of sequences at the site of the P-insertion), *Drosophila* females that are homozygous for *P-lacW* (inserted on the X chromosome) are crossed with males carrying the transposase source P(Δ2-3) (Deak et al., 1997). Random transpositions of the mutator element are then 'captured' in lines lacking transposase activity. Stable, or balanced, stocks bearing single lethal *P-lacW* insertions are made.

More than 41,000 lines are derived, of which approximately one-half are on the third chromosome. Originally some 3100 lethal or strong semi-lethal lines (in homozygous conditions) are identified. During preliminary characterisation unstable lines and clusters of the same mutation event are eliminated leaving 2460 lines to be characterised.

Screening for Mitotic and Meiotic Defects

About half of the mutants in the collection are embryonic lethals. We have carried out cytological screens of the 1155 lines that comprise late larval lethals, pupal lethals, pharate and adult semi-lethals for defective mitosis in the developing larval CNS. This has identified 69 mutations falling into 43 complementation groups that affect all stages of the mitotic cycle. The cytological screens involve examining orcein-stained squashed preparations of the larval CNS to detect abnormal mitotic cells. In lines where defects are

identified, the larval CNS is subjected to immunostaining to identify centromeres, spindle microtubules and DNA for further examination. This leads to clarification of the mitotic defect.

As a set of common functions are essential to both mitosis and meiosis, we then identify mutations resulting in sterility and failed progression through male meiosis. This involves examining squashed preparations larval, pupal or adult testes by phase contrast microscopy. We examine "onion stage" spermatids in the 519 pupal and pharate lethal lines and 463 adult "semi-lethal" and viable lines for variations in size and number of nuclei which provides an indication of whether there have been defects in either chromosome segregation or cytokinesis, respectively. A total of 54 lines of the 519 pupal and pharate lethal lines and 22 of the adult lines show such defects. However, another 67 lines show male sterility without having onion-stage defects. 12 lines showing onion stage defects have been scored as having mitotic defects in the independent cytological screen of squashed preparations of the larval CNS. Twelve further lines with onion stage defects show female sterility and of these, 10 show maternal effect mitotic defects in syncytial embryos. Thus greater than one half of the meiotic mutants scored appear to represent cell division functions specific to male meiosis or have targeted male germ-line specific enhancer elements, thus revealing their meiotic function but in this test not their mitotic function.

Further characterisation of testis preparations of each line by phase-contrast microscopy with and without staining with Hoechst to reveal DNA defined 6 broad categories of meiotic mutants:

8 mutants from the collection show defects in meiotic entry or at early stages in the first meiotic division (MF1-8).

18 mutants (15 complementation groups) show abnormal meiotic spindles (AB1-16). Mutants in this group almost invariably show an associated weak defect in cytokinesis, and 7 show a strong defect in spermatid differentiation. 3 of these mutants

also show mitotic defects in larval brains or in embryos derived from homozygous mutant mothers.

18 mutants (16 complementation groups) also show abnormal meiotic spindles that are strongly multipolar (MUL1-15). Three of these also show maternal effect mitotic abnormalities of multipolar spindles in syncytial embryos.

4 mutants (3 complementation groups) show strong defects at all stages of spermatogenesis from the pre-meiotic stages to spermatid elongation stages (PL1-3). In this respect they resemble the *polo*^{1} mutation.

4 mutants show segregation defects as indicated by spermatid nuclei of heterogeneous sizes (SEG1-4). The spindles appear normal but all have what are either chromosome bridges or lagging chromosomes. One of these also shows a maternal effect.

9 mutants (7 complementation groups) show predominant cytokinesis defects. Two complementation groups also have cytokinesis defects in mitotic cells in the larval brain.

In the Examples below, the designations MF, AB, MUL, PL, SEG or CK are included in the category description where available. Further phenotype information for each mutant described in the results section is provided in the "Phenotype" field. There is considerable overlap between these categories, and it will be of much interest to distinguish between mutants in which the primary defect results in secondary consequences, and mutants that affect more than one aspect of spermatogenesis, as for example appears to be the case with *polo* mutants (Sunkel and Glover, 1988; Carmena et al, 1998).

In the Examples, lines exhibiting mitotic and meiotic phenotypes are categorised generally into four categories:

Category 1 : Failure to complete cytokinesis

Category 2 : Failure to enter M-phase

Category 3: Metaphase arrest

Category 4: Anaphase defect

Category 5: Small Imaginal Discs (Block to Proliferation; see below)

Category 1 phenotypes are exhibited by mutations in Examples 1 to 14; while Category 2 phenotypes are exhibited by mutations in Examples 15 to 19. Category 3 phenotypes are exhibited by mutations in Examples 20 to 30, Category 4 phenotypes are exhibited by mutations in Examples 31 to 53. Mutations in Examples 54 to 74 exhibit a Category 5 phenotype.

Generation and identification of second chromosome mutants having small or no imaginal discs.

In the case of the second chromosome the flies used were from a second chromosome P-element collection established in Szeged, Hungary (Torok et al., 1993). The process of P-element insertion mutagenesis is essentially as described above. 15475 insertions were recovered, of which 2711 were lethal or semi-lethal. After elimination of clusters of identical mutants, 2399 lines representing 1748 independent lethal insertions were recovered. Lines were chosen from the second chromosome collection on the basis of having small or no imaginal discs, to indicate a disruption in cell cycle progression that leads to underdevelopment of the discs. All the second chromosome mutants referred to in the results section are noted under the "Phenotype" field as "second chromosome, small imaginal discs" and comprise Category 5.

Cytological Mapping of the P-Element Insertion Sites

The site of insertion of the P-element in each mutant line was determined by *in situ* hybridisation of P-element DNA to salivary gland polytene chromosomes as described in Saunders et al., 1989. Wandering third stage larvae were dissected and fixed as described and incubated with biotin-labeled DNA made from the *P-lacW* plasmid. After signal

detection chromosomes were stained with Giemsa and examined by microscopy and signals indicating the presence of P elements were assigned to polytene chromosome bands referring to the Bridges map (Lefevre, 1976). In the majority of cases a single P element was detected, only 10% of lines having multiple (two or three) insertions. The site of insertion is given as the "Map Position" field in the results section (for example 77B)

Plasmid Rescue of P-Elements from Mutant Drosophila Lines

Genomic DNA was isolated from adult flies by the method of Jowett et al., 1986, and plasmid rescue from the genomic DNA was performed according to Pirrotta et al., 1986. This allows the recovery of genomic DNA adjacent to the P-element which facilitates the identification of the site of P-element insertion and of genes which may be disrupted by the insertion. Essentially, genomic DNA derived from about 200 flies was digested with a restriction enzyme known to have a site within the P-element (EcoR1 or SacII for cloning sequences to the left of the element, or XbaI, BglII, PstI or BamHI for sequences to the right of the element). The digested DNA was ligated overnight, and plasmids recovered by electroporation of the ligated DNA into *E.coli* XL1-blue competent cells. Appropriate primers from within the P-lacW sequence were used to determine the sequence of the genomic DNA flanking the element (on average, 400 bp of sequence were obtained). The rescue sequences are provided in the results section under the heading "Rescue sequence". Where more than one sequence was recovered, the orientation of each sequence is also given.

Sequence Analysis of P Element Insertion Lines

Sequences flanking the insertion site of the P-element were derived by P element rescue as described above. In some cases sequence was obtained from only one side of the insertion, while in other cases sequences were obtained from both sides of the insertion.

As a first step, each P element rescue sequence was used to search a total database of *Drosophila melanogaster* sequences (database of the Berkley *Drosophila* Genome project) using the BLASTN program (which compares a nucleic acid sequence with a nucleic acid database, (Altschul and Lipman 1990)) with default parameters.

The search may identify a number of different types of match including *Drosophila* ESTs, known *Drosophila* genes and cloned genomic regions.

The ability to identify genes already known to be essential for cell cycle progression using this approach was confirmed, in this example, by the rescue sequence obtained from line 1324/8 which mapped to the 77B locus which was used to search the database. A BLASTN search identified a number of matching *Drosophila* ESTs, a match with the known cell cycle regulatory gene *polo* and a cloned genomic region designated CSC: AC018188. These matches are recorded in the results sections under the field headings "*Drosophila* ESTs", "*Drosophila* gene hit" and "Genomic hit, Accession No.", respectively. Any entries under "*Drosophila* gene hit" are further annotated with "(BLASTN with Rescue sequence)" to show that the match was obtained using the rescue sequence rather than a *Drosophila* EST or genomic clone ORF (see below). Accession numbers of ESTs, genes and genomic clones are provided where known. Genomic clones designations often include the Genbank designation as part of a longer designation. However the Genbank designation is always the code beginning with "AC" and followed by six digits.

Where an EST was identified, this was subsequently used to search using the BLASTX program (default parameters) against databases of sequences from *Drosophila* and Homo sapiens (databases of the National centre for Biotechnology Information (NCBI), National Library of Medicine, National Institue of Health, USA). In the case of line 1104/16, the search identified a known human gene, phosphatidylinositol transfer protein (accession no. P48739) implying a novel function for this protein in cytokinesis. Human Homologues identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "Human homologues" and annotated with "(BLASTX with EST)". *Drosophila* genes identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "*Drosophila* gene hit" and annotated with "(BLASTX with EST)".

Where no *Drosophila* gene was identified using the initial BLASTN search but a matching genomic clone was found (a Bac or P1 clone often in excess of 100 kilobases), a

20 kilobase segment of this genomic sequence (10 kilobases either side flanking the site of the P-element insertion) was subjected to a number of analyses.

If the rescue sequence matched sequences that lie within a known gene present within the genomic clone then these are presented under the heading "*Drosophila* gene hit (BLASTN with Rescue sequence". The known gene sequence was then used in a BLASTX search of a human database (NCBI – see above) to identify any human homologues. These are shown in the "Human homologue" field and annotated with "(BLASTX with *Drosophila* gene)".

If the rescue sequence does not match any sequences that lie with a known gene within the genomic clone then the occurrence of ORFs within the 20 kilobase genomic segment was predicted using the Genscan programme (Burge and Karlin, 1997). Where the P-element was observed to be inserted into the coding region or within the 5' untranslated region (which we defined as within 2 kilobases of the predicted start of the coding region) we assume the P element to be capable of disrupting the expression of the predicted gene. Each predicted open reading frame (or predicted coding sequence) was then used to search *Drosophila* and human databases using the TBLASTN program (compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames) and/or the TBLASTX program (compares a nucleotide query sequence dynamically translated in all reading frames against a nucleotide sequence database dynamically translated in all reading frames) to determine whether the predicted open reading frame corresponded to a known gene. Typically, TBLASTX is only used when no matches are found using TBLASTN.

Where the TBLASTN search found a known *Drosophila* gene, then this is indicated in the results in the "*Drosophila* gene hit" field, annotated with "(TBLASTN with predicted ORF)". The *Drosophila* gene sequence was then typically used to search a human database (NCBI – see above) to identify any human homologues using BLASTX. These are shown in the "Human homologue" field and annotated with "(BLASTX with *Drosophila* gene)".

Where the TBLASTN and/or TBLASTX search found a known human gene, then this is indicated in the results in the "Human homologue" field, annotated with "(TBLASTN (or TBLASTX) with predicted ORF)".

If the TBLASTN and/or TBLASTX search found no *Drosophila* or human genes, then it was assumed that the original ORF corresponds to a novel gene. If the TBLASTN search found no *Drosophila* genes but identified a human homologue, then it was assumed that the original ORF corresponds to a novel *Drosophila* homologue of a known human gene.

Additional Sequence Analysis using the Annotated* D. melanogaster *Sequence (GadFly).

Rescue sequences were also used to search the fully annotated version of the *Drosophila* genome (GadFly; Adams, et al., 2000, Science 287, 2185-2195), using GlyBLAST at the Berkeley *Drosophila* Genome Projects web site to identify the genome segment (usually approximately 200-250 kb) containing the P-element insertion site. The graphic representation of the genomic fragment available at GadFly allows the identification of all real and theoretical genes which flank the site of insertion. Candidate genes where the P-element is either inserted within the gene or close to the 5' end of the gene were identified. In GadFly, the *Drosophila* genes are given the designation CG (Complete gene) and usually details of human homologues are also given. In most cases, this data confirms the data derived from the sequence analysis procedure described above, and in some cases new data is obtained. Where available both sets of data are included in the individual Examples described below. To identify further candidate human homologues, BLASTP (amino acid query sequence against amino acid database) searches with *Drosophila* sequences are used against the human genome project database and also the Ensembl dataset. The Ensembl dataset comprises GeneWise gene predictions using a protein template where possible or Genscan followed by BLAST confirmation via protein, cDNA or EST hits. These are matched using WUBLASTP with default parameters (Altschul et al., 1990, *J Mol Biol* 215, 403-10). The results are filtered to contain only potential homologues. Only matches with the identity of more than 50% and length of more than 50 amino acids are included.

Confirmation of Cell Cycle Involvement of Candidate Genes Using Double Stranded RNA Interference (RNAi)

P-elements usually insert into the region 5' to a *Drosophila* gene. This means that there is sometimes more than one candidate gene affected, as the P-element can insert into the 5' regions of two diverging genes (one on each DNA strand). In order to confirm which of the candidate genes is responsible for the cell cycle phenotype observed in the fly line, we use the technique of double stranded RN interference to specifically knock out gene expression in *Drosophila* cells in tissue culture (Clemens, et al., 2000, *Proc. Natl. Acad. Sci. USA*, 6499-6503). The overall strategy is to prepare double stranded RNA (dsRNA) specific to each gene of interest and to transfect this into Schneider's *Drosophila* line 2 to inhibit the expression of the particular gene. The dsRNA is prepared from a double stranded, gene specific PCR product with a T7 RNA polymerase binding site at each end. The PCR primers consist of 25-30 bases of gene specific sequence fused to a T7 polymerase binding site (TAATACGACTCACTATAGGGACA), and are designed to amplify a DNA fragment of around 500bp. Although this is the optimal size, the sequences in fact range from 450 bp to 650 bp. Where possible, PCR amplification is performed using genomic DNA purified from Schneider's *Drosophila* line 2 as a template. This is only feasible where the gene has an exon of 450 bp or more. In instances where the gene possesses only short exons of less than 450 bp, primers are designed in different exons and PCR amplification is performed using cDNA derived from Schneider's *Drosophila* line 2 as a template.

A sample of PCR product is analysed by horizontal gel electrophoresis and the DNA purified using a Qiagen QiaQuick PCR purification kit. 1µg of DNA is used as the template in the preparation of gene specific single stranded RNA using the Ambion T7 Megascript kit. Single stranded RNA is produced from both strands of the template and is purified and immediately annealed by heating to 90 degrees C for 15 mins followed by gradual cooling to room temperature overnight. A sample of the dsRNA is analysed by horizontal gel electrophoresis.

3µg of dsRNA is transfected into Schneider's *Drosophila* line 2 using the transfection agent, Transfect (Gibco) and the cells incubated for 72 hours prior to fixation.

The DNA content of the cells is analysed by staining with propidium iodide and standard FACS analysis for DNA content. The cells in G1 and G2/S phases of the cell cycle are visualised as two separate population peaks in normal cycling S2 cells. In each experiment, Red Fluorescent Protein dsRNA is used as a negative control. In some cases the phenotype is confirmed by fixing cells on poly-lysine covered slides which are then stained for DNA using DAPI and for tubulin using an anti-tubulin antibody YL1/2 and appropriate fluorescent secondary antibody to visualise aberrant mitoses.

It should be noted that RNAi could not confirm phenotype in all cases. This is to be expected as the method relies on the ability of dsRNA to prevent new protein expression. Consequently, it is necessary that S2 cells express the specific cDNA of the gene in question, and also that the protein is turned over rapidly. It would therefore probably be difficult to sufficiently reduce levels of very stable proteins using this approach.

The layout of a typical entry in the results section is shown below. Not all fields present in the actual results section contain information for each individual *Drosophila* line described.

TYPICAL RESULTS LAYOUT

Line ID	- *Drosophila* line designation
Category	- Description of phenotype
Reversion	- R = revertant, NR = non revertant, ? = not determined
Map Position	- according to the Bridges map (Lefevre, 1976).

Rescue ID
Rescue Sequence
[nucleotide sequence]

Genomic hit, Accession No.

Associated ORF
GENSCAN_predicted_peptide [results of Genscan - amino acid sequence]
GENSCAN_predicted_CDS [results of Genscan nucleotide sequence]

***Drosophila* Gene Hit**
(BLASTN with rescue sequence)

(TBLASTN (or TBLASTX) with predicted ORF)
(BLASTX with EST)

Human Homologue
(BLASTX with *Drosophila* gene)
(TBLASTN (or TBLASTX) with predicted ORF)
(BLASTX with EST)
***Drosophila* EST**

Annotated *Drosophila* genome genomic segment
Annotated *Drosophila* genome Complete gene candidate
Human homologue of Complete gene candidate

Putative function Derived from homologies or Drosophila experimental data

Confirmation by RNAi Description of Facs analysis DNA content profile

A specific example is as follows:

Line ID 1324/8
Category Mitotic defects in brain: metaphase arrest (overcondensation, some circular chromosomes, no anaphases, very high mitotic index, metaphase (or less aligned) with bipolar spindle, no CP190 staining)
Reversion R
Map Position 77B

Rescue ID B1E
Rescue Sequence
GTTTTGCCCATCGATTGCACGAAAACCAAGCACAAAGCGGAGAACGCGCCGA
AACCGTTCGATTTTTTAAATGCCAAAATGAATTGGACGTGAAGCGTCAGCTGA
ATTGGTGTGCCCGTTTCGGTGGCTATCGCACACTTTCTGGTATTTATCGCGGTA
TTTTGTTGAGTGTTGAACAACAAATTCTATGGCCGTTACCCTTTTGAATTTACT
TACTGGCGTTTACTCTGTTCGAATTGAGCGCAATATTTTTTCCTATTGCTCTGC
GCAACACTGTGTTTTAACCGCTATTTATTTGAAAATCTACAAAAACTAACCGTT
TACATTTTTGAAATTTCCAAAAGGGTTTTCCATAAATTGAGTTTTACTAAAACC
AGTCCAACGGTCCAACTTTATATTGTTAGAAGCCCCTTTTCCTAATTTGAATTG
GCTTGCAAACGTTTTCCTGAATTTAAAAATACTGCCACCCTTGTTAATTGCAGG
TTTTCCGAATCCCTGATTTGTTGTTTTAAAAAGAAAATTTATTAGAAACAGCTA
TCTCAACC

Genomic hit, Accession No. CSC:AC018188
***Drosophila* Gene Hit** Polo (X63361)
Human Homologue BLASTX PLK-1 (P53350)
***Drosophila* EST** several including LD11851 (AA392613) which match polo

Annotated *Drosophila* genome genomic segment AE003514

Annotated *Drosophila* genome Complete gene candidate	CG12306
Human homolog of Complete gene candidate	1e-169 1709658 P53350 PLK1_HUMAN SERINE/THREONINE-PROTEIN KINASE PLK (PLK-1)

Putative function	Serine/threonine kinase known to be required for mitosis

Confirmation by RNAi	Reduced G1 and G2/M peaks indicating fewer cycling cells, microscopy analysis of DNA and tubulin staining identified monopolar spindles characteristic of polo mutation in Drosophila.

CATEGORY 1: FAILURE TO COMPLETE CYTOKINESIS

Example 1 (Category 1)

Line ID 1031/14
Category Mitotic defects in brain: cytokinesis defect (polyploidy)
Reversion R
Map Position 74B

Rescue ID 2A3B
Rescue Sequence 1
CCCCGGAACATATGTTCAGTGTGGCCGCAGCAGAGTTGTCAAAACACGCTCCC
CAATGAAATAACCTAAATGTGCCATCACTGTTACTTAACAGTTTCTGTTACTTT
TCTAGCGGCATGTCAAAAAAACAAAAATATAGAAAATGCTAAATATATATTG
GACTAATGTGTTTAAATGTAACTTACACTAGTAACAGATCCCCATTAATAAAA
GCCAAACTCTAAAATTCTGCCACAAGTACTATTTCTCACGTAACACCTTACTA
ACGGATTTCACATGATATCTACGACAAGAAACTGTTTGCTGATATAAAATTGC
TATCACCGCTTTCCGTAAACACTTTTACACTGATGGATTACAAGTTCAATTAAT
ACATCAACTTACCTTAACAATTTTAAGACAACTAACACTCCCACAATTTAATT
CAACCTACACCGCTTGATAATCAGCTGTTCTGTACAAAAAACAATAACACTGT
TAACAACAGCGCACAGTGGATAATACAGTCCTAAAGGCAATATACCCATTTG
GCATTTTT

Rescue ID 2A3S
Rescue Sequence 2
TTCCGGGGAGAATGGCTGCGATTTCGCGTCGGTAAAAATAGCAAATACTCGTTA
ATGTGCTGTGGGAACGCTTCCTCCCCGGCCCCAAAGTGGCCCCGAAGAAAGTGA
GCAAATGTGCGCGCCGCAAGATAGTCGCCGCCGAACAAACGATAGTGACGAAA
GTGATTTAATTCAACTACCAGCACTCCCGCAAATACGATGAGTATGTCGCGCGG
CGGCAACACAACTCTGGACTTGCAGCCGCTCCTGGCGGAGAGCGATGTCGGAA
ACAGGGAGCTGGAGGAGAAGATGGGCGGATCGGCGGATCGGTCATCGCTGCTC
GATGGATCCGGTTCGAAGGAGCTGAGTCACCGGGAACGCGAGGACTCGGCGTT
GTTCGTCAAGAAGATCGGGAGCGCCTTGTTCTATGGCTTGTCCTCCTTCATGATT
ACGGTGGTAAACAAGACGGTGCTTACCTCCTACCACTTCCCCTCGTTCCTGTTCC
TCAGCCTCGGGCAACTTACTGCTAGCATTGTGGTCCTGGGCATGGGCAAAGCGC
CTGAAAATGGTGAACTTTTCCCCTTTTGCAGAGGAATACCTTCGCCAAGATCTTT
CCGCTGCCACTGATATTTCTGGGAAACATGATGTTTGGACTGGGTGGCACAAAA
ACCTTGAGTCTGCCCATGTTCGCAGCCCTACGAC

Genomic hit, Accession No. AC019515

Associated ORF
Genscan ORF1 predicted sequences:>15:31:57|GENSCAN_predicted_peptide_4|373_aa

MSMSRGGNTTLDLQPLLAESDVGNRELEEKMGGSADRSSLLDGSGSKELSHRER
EDSALFVKKIGSALFYGLSSFMITVVNKTVLTSYHFPSFLFLSLGQLTASIVVLGMG
KRLKLVNFPPLQRNTFAKIFPLPLIFLGNMMFGLGGTKTLSLPMFAALRRFSILMT
MLLELKILGLRPSNAVQVSVYAMIGGALLAASDDLSFNMRGYIYVMITNALTASN
GVYVKKKLDTSEIGKYGLMYYNSLFMFLPALALNYVTGNLDQALNFEQWNDSV
FVVQFLLSCVMGFILSYSTILCTQFNSALTTTIVGCLKNICVTYLGMFIGGDYVFSW
LNCIGINISVLASLLYTYVTFRRKRAPDKQDHLPSTRGENV

>15:31:57|GENSCAN_predicted_CDS_4|1122_bp
atgagtatgtcgcgcggcggcaacacaactctggacttgcagccgctcctggcggagagcgatgtcggaaacagggagctgga
ggagaagatgggcggatcggcggatcggtcatcgctgctcgatggatccggttcgaaggagctgagtcaccgggaacgcgag
gactcggcgttgttcgtcaagaagatcgggagcgccttgttctatggcttgtcctccttcatgattacggtggtaaacaagacggtgc
ttacctcctaccacttcccctcgttcctgttcctcagcctcgggcaacttactgctagcattgtggtcctgggcatgggcaagcgcct
gaaattggtgaactttccccctctgcagaggaataccttcgccaagatctttccgctgccactgatatttctgggaaacatgatgtttg
gactgggtggcacaaaaaccttgagtctgcccatgttcgcagccctacgacgcttctctatcctgatgaccatgctgctggagctca
agatcctgggactgcgaccttcgaatgcggttcaggtcagcgtatacgcaatgatcggtggagcgctgctggccgcctctgatga
tctgtccttcaacatgaggggctacatctatgtgatgatcactaacgccttgaccgcctcgaatggcgtatatgtgaagaaaaaactc
gacacctcggagatcggaaagtacggcctaatgtactacaactcgctgtttatgtttctgcctgccctggccctcaactatgttacag
ggaatctagatcaggcgctgaactttgaacaatggaatgactcagtgtttgtggtgcagttcctgctcagttgcgttatgggtttcatc
ctatcgtacagcaccatcctgtgcacgcaattcaactcggcgctgaccaccaccattgtgggatgcctgaaaaacatctgcgtaac
atatctgggcatgttcattggaggcgactacgtcttctcgtggctcaactgtattgggatcaacatcagcgtgctggctagtctgctct
acacgtacgtcacttttcggcggaagcgggctcccgataagcaggaccacttgcccagcacccgcggcgagaatgtctag

Human Homologue	(TBLASTN with ORF1): KIAA0260 gene (D87449) and putative Sqv-7-like protein (AJ005866)
***Drosophila* EST**	CK00510 (AA140776)

Annotated *Drosophila* genome genomic segment	AE003524
Annotated *Drosophila* genome Complete gene candidate	CG3874 – novel glucose-6-phosphate transporter
Human homologue of Complete gene candidate	EMBL:D87449 protein KIAA0260_id:BAA13390 gi:166578 Similar to a C.elegans protein encoded in cosmid C52E12 (U50135) and Ensembl predicted gene ENSG00000024527 Clone:AL133320 Contig:AL133320.00001 8.10E-95

Putative function Sugar modification protein similar to proteins involved in Drosophila cytokinesis and signalling

Confirmation by RNAi Marked increased G1 and S peak indicating mainly arrest in G1

Example 2 (Category 1)

Line ID	1066/5
Category	Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects. (Seg-01/62)
Reversion	?
Map Position	89B

Rescue ID F9E

Rescue Sequence

GTATACCATTAGAGAATATGATGAAGAAGGACTGTAAGAAGATCCTTCAGTG
AATTTGACTGCTGACGTCGATCGGAACTTGCTGCGCTGACGTACAAAATCGCG
AAGTGAATAAATAATATGGATGAGACCCTGTTTCGCCGACATATACAATAGTG
CTCAAGACCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATATTT
CTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTTCT
TCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCACAAG
CATTAATTTGTCATGATTCTCTTAAGCGTGCACTTTATCTGAAAGTCTGAACAG
CTGGCTGCGAAATGGATCCCCGGGATTGGAGATGGCAAGTAAATCTGTCCTCG
CTACAAACAAGTGGGCACCACTGGGCATTCGGGGAATAGGGATATGGGTTGG
GAATGGGGATATATTGTGGCATTGGCGAAAGGTCGCTATGC

Genomic hit, Accession No. CSC:AC019750

Associated ORF

>16:04:57|GENSCAN_predicted_peptide_4|418_aa
MKPIPNESKGTLAAVGDATVVHDVCTLFAVELDPYLRSSMGMRTRRAQSGALLL
QLLAVADGGFAAHICACKCRLRLPHVTCCCNRNPFKATAKAKGQAVSSTKPNQL
CFHGCCGWIITTKGETFTENSPSIMSGFAWERHSLGECVVVAGTEQILLIGRTLIGR
MSHTQTDSTSPFVVDCHSQLCGSKCKCICVSVGFCVRPSCQRFDMKIVWANLAM
QKRFLLGAAIADMCCRNSVIWCKLQLDPVKPIDERADGSGLALVTKVCDNNNIV
HYVVVAGVTGSQSRSRLQPLRSGQNESTEQWPRTKGGEGGFNNNSRNNKHSAPT
QEQQELWQKQLLQDQRDDCHASGSFQSASFAETRSFTFDDTTAHSEFCFRTRAEK
RRILVLLETSIKLKPDKYATSGHTRRCAIGLLHSII

>16:04:57|GENSCAN_predicted_CDS_4|1257_bp
atgaaacccattcccaacgaatccaagggaacccttgcggcagttggagatgctactgttgttcatgacgtgtgtactttgtttgccg
tagagcttgatccctatctcaggagcagcatgggaatgaggacgcgtagagctcaaagcggcgctctgttattacagctccttgcg
gttgccgatggaggttttgctgctcatatttgtgcctgcaagtgtcggcttcgtttgccacatgtcacatgttgctgcaaccggaatcct
ttcaaggcaactgcaaaagcaaaaggtcaggcggtcagctccactaaaccaaaccagctttgctttcacggctgctgtggctggat
aattactaccaaaggtgaaacgttcaccgaaaactcgcccagcatcatgagcggttttgcgtgggagcggcatagccttggtgagt
gcgtggttgtggctggaacggaacaaatcctgctgattggcaggacattgattggccgcatgagccatactcaaactgattcgacc
agcccctttgttgtcgactgtcactcgcaactgtgcggctccaagtgcaaatgtatctgtgtatctgtaggtttctgtgtgcgcccgtct
tgtcagcgctttgacatgaaaatagtttgggccaacttggctatgcaaaagcgatttctattaggagccgccatcgccgacatgtgct
gccgaaattcggtgatttggtgcaaactgcagctagatccagtcaagccaattgacgaaagagccgacggcagcggtcttgcact
ggttaccaaagtatgcgataacaataacatcgtccactatgtggtcgttgctggggttacgggcagtcagtcacggtcacggctgc

aacccctccgctccggccaaaacgagtccacagaacaatggccaaggacgaagggggggggaggggggattcaataacaaca gcaggaacaacaaacattctgctcccacgcaagagcagcaggaactgtggcaaaaacagctgctgcaggatcaacgagacgat tgtcatgccagtggaagcttccagtctgcgtcattcgcggagacgcgtagtttcacgttcgacgacacaaccgctcacagcgaattt tgttttcggactagagctgagaaacggcgaattttggtgcttctggaaacatcgattaaactaaaacccgataagtatgcgacaagc ggtcacactcggcgatgtgcgataggattgctgcattcgattatatag

***Drosophila* Gene Hit**	rescue sequence: mitotic heterochromatin fragment clone CH(2)6 (L36595) and subtelomeric heterochromatin repeats (L03284). TBLASTN with ORF1: nebula (nla) (AF147700)
Human Homologue	BLASTX with nebula: Down Syndrome candidate region 1-like protein 2 (AF176117)
***Drosophila* EST**	rescue sequence: CK01138 (AA141069)

Annotated *Drosophila* genome genomic segment	AE003712
Annotated *Drosophila* genome Complete gene candidate	CG6072 - nebula CG6046 – sap18

Human homologue of Complete gene candidate	CG6072- 8e-36 'ZAKI4 a thyroid hormone responsive gene in human skin fibroblasts' also known as DOWN SYNDROME CANDIDATE REGION 1-LIKE 1; DSCR1L1 EMBL:D83407 protein_id:BAA11911 gi:143504 CG6046- 3e-45 2108210 (U96915) sin3 associated polypeptide p18 [Homo sapiens] and gi5032067 C7E479FFE9CA5774 |ref|NP_005861.1| sin3-associated polypeptide, 18kD [Homo sapiens] (1.90E-43)

Putative function Nebula unknown function, Sap18 transcription factor

Confirmation by RNAi Both show reduction in G1 and G2/S peaks indicating fewer cycling cells

Line ID	234/50
Category	Meiotic defects in testis: cytokinesis defects, abnormal spindles. (Ab-02/12)
Reversion	R
Map Position	89B

Rescue ID 2C5E

Rescue Sequence

GTTTGACTGCTGACGTCGATCGGAACTTGCTGCGCTGACGTACAAAATCGCGA
AGTGAATAAATAATATGGATGAGACTCCTGTTTCGCCGACATATACAATAGTG
CTCAAGACCCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATAT
TTCTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTT
CTTCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCACAA
GCATTAATTTGTCATGATTCTCTTAAGCGTGCACTTTATCTGAAAGTCTGAACA
GCTGGCTGCGAAATGGATTCCCCGGATTGGAGATGGCAAGTAAATCTGTCCTC
GCTACAAACAAGTGGGCACCACTGGGCATTCGGGGAATAGGGATATGGGTTG
GAAA

Drosophila **EST** rescue sequence: CK01138 (AA141069)

All other entries as for 1066/5.

Example 3 (Category 1)

Line ID	1104/16
Category	Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, high polyploidy)
Reversion	R
Map Position	92A

Rescue ID B5P
Rescue Sequence 1
CTCCGGACACGCAGTAGCTAAATAACAAACTCATTACTAGTATATTACTGCCG
CCGATTTGCAAGCGCGTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGT
TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT
GATATTCCGCCCGCTGTGTGTGCGTGTGTATTTGCAAGAGAGTGTGTGTGTGT
GTGTGCATATGACTCGTGCGTTTAGCCGACAATTGGAGAAAAAGCATTACCAA
TCCCAATTGGCTAACTAAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGT
GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG
ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT
GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

Rescue ID B5E
Rescue Sequence 2
GTCCGGAGCGGAGCTAAAGTTCGATGTTCGTGCAAAACACTTCGATTCCGATA
GGCGGATGCTATCGATTTCGGCGATGCCCGTTGGTCACACTTGGTGGTGGGCG
CTGCCCGTCGCCGACTATCGATAGCACAAGCGGGTTATTTAGGTGTGCGCAGC
TTGTAAGGGTGACTCATGCTGTTAAAATTATTATAAAAAGTTAATGAATATAA
TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA
TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG
TTTTTGAAATGTGAAAATGTGGGTTACCCCCAATTCTTATTCGAAATTAAATAA
CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTTGT
CTAGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC
TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA

Genomic hit, Accession No. AC006589
Associated ORF
Genscan: ORF1 predicted sequences
>/tmp/aaaaainga|GENSCAN_predicted_peptide_2|850_aa
MATRGANVIWFRHGLRLHDNPALLAALADKDQGIALIPVFIFDGESAGTKNVGY
NRMRFLLDSLQDIDDQLQAATDGRGRLLVFEGEPAYIFRRLHEQVRLHRICIEQDC
EPIWNERDESIRSLCRELNIDFVEKVSHTLWDPQLVIETNGGIPPLTYQMFLIRCTH
HNGDVNGDEDTGEGEGTGGRIDWAKEGACWRAGNSDEQECQACQSVSSVIMM
VLQYSNNPAHHCQLLECLMTLKHNVVKDILCVVAYGTAVSRTSAAKLLFYYWP
AFNANLFDRKVLLSKLTNDLVPFTCQREHCPNSGNAEAAKVCYDHSISIAYAPDC
PPPLYLCIECANEIHREHGSLEFGDILHPMQQVSMVCENKNCRSNEKSAFSICFSTE
CASFNGNHPIRYCSQCHSNRHNSRRGGDHVVHRSLQPAWQMDPEMQMHMVESV
VSLLREAKPLNFEPGKESSSSESKKNGSGITADNISLEERQRLGRYGIWLLVGRCTP

TADTPVEVLGRILSMLFHWFHVTAYSYDGFISCLVPHPPEYARVGGHWETLASRT
SHLKEGLQRLICLVPYEVITSEIWDYVMPHWMEAITNDVAEKELNELKIVLSKILD
PEMSPLGFDAKTMYNFVAIRFEKTTAKVQQQALHWLQILTKLEILIPLVQLFAMF
GDGVRIMKYGIQHELMREKDAQSQSLAKAPKTPCKESKETKADMANPPRPPVVE
DDSGNTSAISDDEAPTNRHTEFSTDAEHNLTCCILMLDILLKQMELQDVEQHMGI
HTSVCENVSRLIKCMVTAARVGLSSHVCALKVPIEDIIEEEKSSRKSPPESDKEKTR
DRDVSLSMAPLPIPLGPLGGFADP

>/tmp/aaaaainga|GENSCAN_predicted_CDS_2|2553_bp
atggccacgcgaggggcgaatgtgatttggtttcgccatggattgcgcctccatgataat
cccgctctattggccgccctcgccgataaggatcagggtatagccctaattcccgttttcatattcgatggagagagtgcaggtacc
aagaatgtgggttacaatcggatgcgtttcctcctggactcgttgcaggacatcgatgatcagctacaggcggcaactgatggacg
tggacgcctcctggtcttcgagggcgaaccggcttatatcttccgccggctacatgagcaagtgcgtctgcacaggatttgcatag
agcaggactgcgagccaatttggaatgagcgcgatgaaagcatccgttctctatgtcgggagctgaatatcgactttgtcgagaag
gtatcacacacgctttgggatccgcaattggtgattgagaccaatggtggcattccaccgctgacctaccaaatgttcctgatacgct
gcacgcaccacaatggagatgtgaatggggatgaggatacgggagaaggagaaggaaccggcggaaggatcgactgggcta
aggaaggggcctgttggagggcgggaaactccgacgaacaggaatgtcaggcctgccaatcagtgtcctcggtcatcatgatg
gtgctccagtactccaacaatccagcgcatcattgccagctcctggagtgcctgatgactcttaagcacaatgtcgtcaaggacatc
ctctgcgttgtggcatacggaaccgctgtttcccgcacctcggctgccaagctgctcttctactactggccagcctttaacgccaatc
tgttcgatcgcaaagtcctactctccaaactaaccaatgacctagtgcccttcacctgccaacgggagcactgtccgaactccggg
aatgcggaggcagcaaaggtgtgctacgaccacagcattagcatcgcatacgcgcccgattgtccaccgcccctttacctgtgca
tcgagtgcgccaacgagattcatcgggagcacggaagcctggagttcggcgacattctgcatcccatgcagcaggtatcgatgg
tgtgcgaaaacaagaactgtcgctccaacgagaagtccgccttctccatctgcttctccacggagtgtgccagcttcaatggcaac
catccgatccgctactgcagccagtgccacagtaataggcacaattcccggcgaggtggcgatcacgtggtccatcgcagtctgc
agcccgcctggcagatggatccagagatgcagatgcacatggtggagtcggtggtaagccttctgcgagaggcgaagccacta
aactttgagcccggcaaggagtcctcgtcgtccgagtccaaaaagaacggctccggcatcacagctgacaatatttctctggagg
aacgccagagactgggacgctatggtatctggctactggtgggtcgctgtacacccactgcagatactcccgtagaagttctggg
caggattctgagcatgctcttccactggtttcatgtaaccgcttactcatacgatggttttatatcctgcctggtgccacatcccccgga
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aggaactgaacgagctgaagattgtgctcagcaagatcctcgatccggaaatgtcgcctctgggctttgatgccaaaaccatgtac
aactttgtggccattcgatttgagaagacaacggcaaaggtgcagcagcaggcactccactggctgcagatcctcaccaagctgg
agattctcattccactggtccagttgttcgccatgttcggcgatggtgttcgcataatgaaatacggcatccagcacgagctgatgcg
cgagaaggatgcccaatctcagtccctggccaaggctcccaagaccccgtgtaaagagagcaaggagaccaaagcggatatg
gccaatccgcccaggcctcctgttgtcgaggatgactctggtaatacgtctgccatttcggatgacgaggcgcccacgaatcgtca
cacggaattctccacggatgctgagcacaatctcacctgttgcatcctcatgctggacatacttctgaagcaaatggaactacagga
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gggtctcagtagtcatgtctgcgccttaaaggttcccatcgaggacatcattgaggaagaaaagtcctcgcgcaaatctccacccg
aatccgacaaggaaaagacccgtgatcgagatgtttccctctcgatggctccactacccattccgctgggacctttaggaggatttg
cagacccttaa

Human Homologue BLASTX with EST: Phosphatidylinositol transfer protein (P48739)

***Drosophila* EST** SD01527 (AI530804), GH18602 (AI387906)

Annotated *Drosophila* genome genomic segment AE003725

Annotated *Drosophila* genome Complete gene candidate CG5269 – vib PIP transfer protein

Human homologue of Complete gene candidate 1e-90 1346772 P48739 PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM

Putative function phosopholipid transporter involved in lipid metabolism

Confirmation by RNAi Slight reduction of G1 and increase in G2/M peaks indicating arrest in G2/M

Line ID 418/32
Category Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant.
Reversion ?
Map Position 69C

Rescue ID G2E
Rescue Sequence
AGCTAAATAACAAACTCATTACTAGTATATTACTGCCGCCGATTTGCAAGCGC
GTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGTTGTACGTCATCACTT
AAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATTGATATTCCGCCCGCT
GTGTGTGCGTGTGTATTTGCAAAAGAGTGTGTGTGTGTATGTGCATATGACTC
GTGCGTTTAGCCGACAATTGGAGAAAAAGCATTAGAATCCCAATTGGCTAACT
AAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGTGCGGGCGCAGCGATT
TGGCAGCGAAACAAAAACACCAAAGTGTTATTGGCAGATATATATGTTAATTA
AATATNAAAAAGTGCGTGCGAA

Genomic hit, Accession No. AC006589

***Drosophila* EST** SD01527 (AI530804), GH18602 (AI387906)

Rest of results same as line 1104/16

Example 4 (Category 1)

Line ID	1285/1
Category	Meiotic defects in testis: cytokinesis defects
Reversion	?
Map Position	85D1-5
Rescue ID	D8E

Rescue Sequence

GTTCGCAAAAAATATATCTCACCGTGAGTGCGAAAGAGAAAAAGAGAAGCGG
AGAGGTGGAGAGCAAGTGGACATGAATCGTCGAGAGTCAGAGAGAGAGAGG
TGGAGAGGGTGAGCAGCTGTTGTCTGACAATAACATAATCAGCAACAATTTAT
GCTGTTTAAAAAGAGCAAGAGAAACGCTAATGAAGGGGAACACGGGCAGGGT
CAGGGGTTGGTGGATCCCCTACATATCTCTCTCTTTCACCGCCCCCGCTCTGGC
ACCCTCTCTGTCGCTCTCCCATTAGCCGCACACGTGCAAGCTTAGCATTCTATC
TGTCTGTCTCTGTTTGTGTTTGTTTGCTAAGCCGAATTCT

Genomic hit, Accession No. CSC:AC014256

Associated ORF

Genscan ORF1 predicted sequences

>/tmp/aaaaakfaa|GENSCAN_predicted_peptide_1|702_aa
MIQRCVVLLWIVCFCDLFLGLLFLKRKRNAHTPPPPPQFTTYRHLLCYCFRNGEIM
ANICLSRLSVLEEIVLLLRVPCAFYFVDYYYVPCLLSVLSESFLYHDQLKVFNRTK
QQHQQQQQQQQQLYQQHQQQQQHYGPPPPYFQQLHQQHQQQQQQQQQQ
HQQHMKFLGGNDDRNGRGGVGVGTDAIVGSRGGVSQDAADAAGAAAAAAVG
YVFQQRPSPGGVGVGVGGVGGGVPGVGAVGSTLHEAAAAEYAAHFAQKQQQT
RWACGDDGHGIDNPDKWKYNPPMNPANAAPGGPPGNGSNGGPGAIGTIGMGSG
LGGGGGGGAGGGNNGGSGTNGGLHHQSMAAAAANMAAMQQAAALAKHNHMI
SQAAAAVAAQQQHQHPHQQHPQQQQQQQAQNQGHPHHLMGGGNGLGNGNG
LGIQHPGQQQQQQQQQQQQHPGQYNANLLNHAAALGHMSSYAQSGGSMYDH
HGGAMHPGMNGGMPKQQPLGPPGAGGPQDYVYMGGQTTVPMGAAMMPPQNQ
YMNSSAVAAANRNAAITTSTAKKLWEKSDGKGVSSSTPGGPLHPLQIPGIGDPSS
VWKDHTWSTQGENILVPPPSRAYAHGGASDTSNSGNAGILSPRDSTCAKVVEYVF
SGSPTNKDSSLSGLEPHLRNLKFDDNDKSRDDKEKANSPFDTNGLKKDDQVTNSN
GVVNGIDDDKGFK

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gcagcagcaactctatcagcaacatcaacagcagcagcagcaacattacggtccaccaccgccctactttcaacagctacacca
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aatgaacggcggcatgcccaagcaacagccattgggtccacccggagccggaggaccccaggactatgtctacatgggtggc
cagaccactgtgcccatgggagccgcaatgatgccgccacagaatcaatatatgaacagctctgctgttgcagctgccaatcgga
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gcatttgcggaatctaaagtttgacgacaacgataagtcacgcgacgataaggagaaagcaaactctccgtttgacacaaacggtt
tgaagaaagacgatcaggtcacaaactcaaatggtgttgtcaacggcattgacgatgacaagggcttcaagtga

***Drosophila* Gene Hit**	TBLASTN of ORF1: pumilio protein (L07943)
Human Homologue	TBLASTX with pumilio: Soares fetal heart NbHH19W Homo sapiens cDNA clone (W77820)

Annotated *Drosophila* genome genomic segment	AE003681
Annotated *Drosophila* genome Complete gene candidate	CG9755 – pumilio RNA
Human homologue of Complete gene candidate	1e-154 1944416 dbj|BAA19665| (D87078) similar to D.melanogaster pumilio protein (S22026)

Putative function	Putative RNA binding protein which is localised to the cytoplasm. Wild-type allele of pum involved in development of the abdomen (embryos) and of the imaginal discs (larvae or pupae), perhaps having a function in signal transport.
Confirmation by RNAi	Only wild type profiles observed

Example 5 (Category 1)

Line ID	1389/1
Category	Meiotic defects in testis:segregation defect, cytokinesis defect (Ck-09/32)
Reversion	NR
Map Position	93B4-8

Rescue ID 2C9P

Rescue Sequence 1

GTTCGGGGTGTGTGCGTGCTTGCGAGTGTGCCTGTGTGTGTGTAGGAAAGGAG
CAAGAAGCAGCAGCAGCGGCAGCAGTAGAAATAGCAAAAGGAGGCAGCAAC
AACAATAAGCTAGAGAAACCGCCAGCAGCAGCCCCCTAATAAAGAGCAGAGA
AAAAAATGAGTTCAAGTTGTGAAAGGTGTGTGCCGTTACACTACAAACTACAA
CACCACCATCAGCGGCAGCAAAGAAATACAACAACAAATACGGCAATCTCCA
GACAACGCGAATGTCGAAATTGTGTATACAATTTATTAAGAAAGCAAGAGCA
GCAACAACAATGACCAGCTGCAGTTCATCAGCGGTGTCCTCCTGAATGCCGCT
GTCGTCGTTGGTGTCTGCCACCGGCGGTTCCTCAATAATAAGGGCAGGAGGAG
CTGCTTAGGTGCACACAATGTAGTTTGGCTTGGTGAATGCTTCTCTTTTTGTTG
CTGCTGGCGCATACGTTCCTCTTCTCCCCTCATGATCTCAGTTGTCTGCATCGA
TGAGCCGCCACCAACGGTGGCTTCTTCTGCTCCTCTTTGGCAACGGACTGCTG
CAGTCTTGCCAGAATTTTTCCTAAAATACTGAGCTTCAACTTGGTCTGCTTGGT
AATGGTATACCATAAGCCATGGACTTGATGCCCCTACAAAGCTCTGTGATTTG
AAATGGGATGCA

Rescue ID 2C9E

Rescue Sequence 2

CCCCGAACGCACTTTATATATATAAATATATATATTATTTTCTTTCACTTATTTT
CGTTTCGGCCGCGACAGCGAATATGCAATTTTCCTCTCAATTGATTTTTTTACA
CACTCGCACTCCTTTTCACATGCGTGCAGTTTATGTTGCTATTGCTGCTACTGC
TGCTGTTGTTGTTATTGTTGTTCTGGCTGCCGCTGCAGTGCAACTTGTAACACT
TTCACATTTATGACATAATGCACTGGCCATATTTTTGCTTGGCTCTCCGTTTGT
GCAACTGCATGTTCCCAGTGCTTTTTTAATATTTATGCTGCAGTGCGTGCAAAT
TCGAACGCGAGACGATCCGCTTTTCGCTGCATCTATGCGCTGAAGATGTGCTG
CAGTCGATGGGCTCGTCGATAGTGGGAAGGCTCGGTGCCGGCACTATCGATTC
CCAACACCATACGATAATATCGGCTAAAGTTATCAATATCGAAGTTTACTATA
TTTCGGGTTTTTACGTTTTAAATCTACCTTATCAACATTTTTGNAAGAAGTAAA
AAGTAGTTCTCTTATGGATGCATC

***Drosophila* EST** several including LD10379 (AA816796)

Annotated *Drosophila* genome genomic segment	AE003733
Annotated *Drosophila* genome Complete gene candidate	CG3421 - novel protein with weak homology to myosin

Human homologue of Complete gene candidate	Ensembl predicted Gene:ENSG00000071333 Clone:AC022505 Contig:AC022505.00011 5.60E-37 (predicted protein with Core domain in kinesin and myosin motors ENSG00000087179)

Putative function Possible novel motor protein involved in cytoskeleton organization

Confirmation by RNAi Marked reduction of G1 and G2/M peaks indicating fewer cycling cells

Example 6 (Category 1)

Line ID	293/9
Category	Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, very high polyploidy)
Reversion	NR
Map Position	66B

Rescue ID 2G5E

Rescue Sequence
GTACAAACGAATTATTTGTCTCCTTGTGCGTTCGTTTTATTGTGTTTCGAGTTCT
GTTGGTGTGTGTTTTTGTGTATGTTCCACGAGTTGTTCGCATTAAAAAATTAAC
TGCAGAAGATCCATGGAAATGGAGACCATTGAAGAGCAATCGAAGTGCGGTG
AGTACTGAAAGAGGGCGCGGGGCGTGGCAGCTCCAAATGGCCGGCGAATTTA
TCATTTTTCAATGTCGTCCAAAGGGGTTGGGTACGGGGTAAAACCACATTCGG
GGCCAAAAGATCCTCATAAAAAATGTCGCTGCCAGCAAATGCAAAAAATAAA
ATAAAATAAGAACGACTATAAGTACATCTTTGTGTGTATTTGTGTGACTAAAA
AAGCAACGGCATCGTGTCGCANATATTTTAATCTTTNTTTCTGAATTTATTTCG
GTGTACAAAATATTTATCGCATAAATGCGAAATGCCTCCCTCTCTTCATCATCG
T

Genomic hit, Accession No. AC008303

Associated ORF
Genscan ORF1 predicted sequences >20:53:38|GENSCAN_predicted_peptide_3|261_aa
MMDNDDALLNNGGPQSGAETVYGTEDNNMVMSEKCRIFPATQRTGFVGATFSG
VLLLDLGALQHCDVIRIDVNIATLEQIKRERQEELAARERIRAQIAADRAEQAQRF
NTPDISSTTNSVAATAASNVITTDASVSSVDETRLQIRLPGGIQRTKSFPAGEVLAT
VRVYVRNEMLAASDVRDFTLATSYPRREFQTEDEVKTLNELNLVPNAVVLVLTK
EQVNPADDQTAKRSASTKRTKTHRHKRQLMADEPQSDHYKN

>20:53:38|GENSCAN_predicted_CDS_3|786_bp
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atggtcatgtcggagaagtgccgcatattcccggcgactcagcgtactggatttgtgggcgcgacgttttcgggagtgctgcttctt
gatcttggtgccctccagcattgtgatgtgatccggattgatgttaacattgcaacgctggaacagattaagcgtgagcgtcaggag
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cgaggctgcagatccgactacccggtggcattcagcgcaccaaatcctttccagccggcgaggtgctggctaccgttcgtgtcta
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aggacgaggtcaagaccctgaacgagctaaatctagtgcccaatgcggtggttctggtgctgaccaaggagcaagtgaatccag
ctgatgaccagacagcaaaacgatcagcaagcaccaaacgcacaaaaacacacagacacaagcggcaattgatggcagacga
gccacaatctgaccattataaaaactga

***Drosophila* Gene Hit** rescue sequence: pebble (rho1 GTPase exchange factor) (AF136492)

Human Homologue BLASTX with pebble: KIAA0337 (AB002335)

***Drosophila* EST** SD09146 (AI542703), SD01796 (AI530981)

Annotated *Drosophila* genome genomic segment	AE003557
Annotated *Drosophila* genome Complete gene candidate	CG8114 - pbl pebble rho1 GTPase exchange factor
Human homologue of Complete gene candidate	2224615 dbj|BAA20795| (AB002335) KIAA0337 [Homo sapiens (3e-21) also mouse homologue 3e-95 42359 transforming protein (ect2) - mouse >gi|293332 (L11316) ect2 [Mus musculus]

Putative function A guanyl-nucleotide exchange factor involved in signal transduction which is localised to the mitotic anaphase. pbl is required for the formation of the contractile ring and the initiation of cytokinesis in Drosophila

Confirmation by RNAi Slightly reduced G1 and G2/M peaks indicating fewer cycling cells

Line ID 542/3
Category Mitotic defects in brain: cytokinesis defect (very high polyploidy)
Reversion NR
Map Position 66A
Rescue ID 2A1E
Rescue Sequence
GTCCAGTTAATGAAAGTAAACGAATCGAGTACAAACGAATTATTTGTCTCCTT
GTGCGTTCGTTTTATTGTGTTTCGAGTTCTGTTGGTGTGTGTTTTTGTGTATGTT
CCACGAGTTGTTCGCATTAAAAAATTAACTGCAGAAGATCCATGGAAATGGA
GACCATTGAAGAGCAATCGAAGTGCGGTGAGTACTGAAAGAGGGCGCGGGGC
GTGGCAGCTCCAAATGGCCGGCGAATTTATCATTTTTCAATGTCGCCCAAAGG
GGTTGGGTACGGGGTAAAACCACATTCGGGGCCAAAAGATCCTCATAAAAAA
TGTCGCTGCCAGCAAATGCAAAAAATAAAATGAAATAAGAACGACTATAAGT
ACATCTTAGTGTGTATTTGTGTGACTAAAAAAGCAACGGCATCGTGTCGCANA
TATTTTAATCTTTTTTTCTGAATTTATTTCGGNGTANAAAATATTTATCGCATA
AATGCGAAATGCCTCCCTCTCTTCATCATCGNTTCCCCTNACTCTCCCTCTCTT
CGCCCGACACTGTACCGACGCAAGAAGAAC

Genomic hit, Accession No. CSC:AC018042
***Drosophila* EST** SD09146 (AI542703), SD01796 (AI530981)

rest of results same as line 293/9

Example 7 (Category 1)

Line ID	229/30
Category	Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic: Ck05/07)
Reversion	?
Map Position	91F
Rescue ID	A7E

Rescue Sequence
TCTTGGCCAAACAACGCGAGCAGCTGATGTCGCATGGTGGGAAAATGAGGGT
GGCGCGAGTGGAAGTTGCCATATCGCTGCGATCACAAGCAGCAAATATGGAA
GATTAAGCGGAAAACGAAAGACAAAATAATTACAATCAAACAACCGAATTAT
AAAAAGAAAATGGTTTGTCCTCCGAGTTCGTTTAAATATGCTTATCTACGTATC
AATTAAAAAAACCGTAGAAAGAAATTCACGATTCACCCTAATCTAGCTAAGA
CACCAACCAAAAATTTCCGATTTACTTTCAGTTGAAGTTGTTGTTACACACTTT
TCTTGTCGATGTTTTGAAGCGCCCATTGAAATTGATCATTTGAATGTTTTTCCA
AATTACCCACATCCATTACAATAAATTTAAATTGCTTATTATTTGATTTTTACT
TGGGAAAATCCCGTTGCCAAATTGGAATTACAATTCCAGCTTGGAATCCGTCA
AACTTTACAACATAAACTTATTGTTCTTTTCCGGACAATGCTTCCA

Annotated *Drosophila* genome genomic segment	AE003686
Annotated *Drosophila* genome Complete gene candidate	CG6284 - novel protein possible sir2 family of transcriptional regulators/telomeric silencing
Human homologue of Complete gene candidate	gi7706710 0268A424791DE5BF |ref|NP_057623.1| sir2-related protein type 6 [Homo sapiens] (1.10E-74)

Putative function Putative transcriptional regulator

Confirmation by RNAi Complete loss of G1 and G2/M peaks indicating fewer cycling cells

Line ID	1104/16
Category	Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy)
Reversion	R
Map Position	92A

Rescue ID B5E

Rescue Sequence

GTCCGGAGCGGAGCTAAAGTTCGATGTTCGTGCAAAACACTTCGATTCCGATA
GGCGGATGCTATCGATTTCGGCGATGCCCGTTGGTCACACTTGGTGGTGGGCG
CTGCCCGTCGCCGACTATCGATAGCACAAGCGGGTTATTTAGGTGTGCGCAGC
TTGTAAGGGTGACTCATGCTGTTAAAATTATTATAAAAAGTTAATGAATATAA
TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA
TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG
TTTTTGAAATGTGAAAATGTGGGTTACCCCCAATTCTTATTCGAAATTAAATAA
CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTTGT
CTAGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC
TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA

Rescue ID B5P

Rescue Sequence

CTCCGGACACGCAGTAGCTAAATAACAAACTCATTACTAGTATATTACTGCCG
CCGATTTGCAAGCGCGTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGT
TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT
GATATTCCGCCCGCTGTGTGTGCGTGTGTATTTGCAAGAGAGTGTGTGTGTGT
GTGTGCATATGACTCGTGCGTTTAGCCGACAATTGGAGAAAAAGCATTACCAA
TCCCAATTGGCTAACTAAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGT
GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG
ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT
GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

other results same as 229/30

Example 8 (Category 1)

Line ID	343/5
Category	Mitotic defects in brain: cytokinesis defect (very high polyploidy, chromosomes entangled?)
Reversion	NR
Map Position	75B

Rescue ID C6E

Rescue Sequence
GGTTTCGAGTTCGTTCGGTTTCGGCCTCTCCGTTCGGCTCTCTCTCGCCATCCC
GCTGCCGCACACATTGGCCTCTCTCTCGCAGCTCCACATTCGAAGGTGGCTGA
CCGAAATGTGGGTCACGACAATGGCGGGGTTCGTTGAACTGAACCACCGCCG
CAGTCGCTGCCGTGCTCGCTGCTCTGCCTCTGCTGACGTCGTTAACGTTTTGGG
GCTTTCGGTTACGTAGCTCGTGTGCGAGCGAGAGGGGCTACTAGAGGGACTGC
GACACACAAGTTGTGTGCATTTTTTGGCCCCAAAAAATCACAATGGGCACAAA
ATATTATTTAATACATCACATAATTGTTTAATCATCTGGCTGGAAAGTGTCGAG
TTCATCGAACTGCCAGCGATTGACAAATTGCGATTTTCAATGCGGCAAAAATA
TTTACTCAAGCAAATTGTTTGCACTTCGTTAATTAGGCGGGGAGTGCCGCCAA
ATTGGGTCATATTGCAGAAGTATCCAAGAAGTTGGAGAAACAAGCTGCTTAA
ACATTAATTAACACACACCTAAATGGATACATTTGCTACAAACAATTATAAAT
GTTACCCTTATATTAATTTTCAAATTTCTAAATAATCAA

Genomic hit, Accession No. CSC:AC015427

Associated ORF
Genscan ORF1 predicted sequences
MVCAMQEVAAVQHQQQQQQLQLPQQQQQQQTTQQQHATTIVLLTGNGGGNL
HIVATPQQHQPMHQLHHQHQHQHQHQQQAKSQQLKQQHSALVKLLESAPIKQQ
QQTPKQIVYLQQQQQQPQRKRLKNEAAIVQQQQQTPATLVKTTTTSNSNSNNTQT
TNSISQQQQQHQIVLQHQQPAAAATPKPCADLSAKNDSESGIDEDSPNSDEDCPN
ANPAGTSLEDSSYEQYQCPWKKIRYARELKQRELEQQQTTGGSNAQQQVEAKPA
AIPTSNIKQLHCDSPFSAQTHKEIANLLRQQSQQQQVVATQQQQQQQQHQHQQ
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HQRLDSSQLNYLCQKFDEKLDTALSNSSANTGRNTPAVTANEDADGFFRRSIQQK
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PSKNSTVNQINSKLELGNSNEMK

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cagcagcagacaacacagcagcaacatgcaacaactatagtgctgctgacgggcaatggcggcggtaatctgcacattgtcgcc
acaccgcaacagcatcagccgatgcatcagctccaccatcagcatcagcatcagcatcagcaccagcagcaggccaagagcc
aacagctgaagcaacaacactcggcgctggtcaagttgctggagtcggcgcccatcaagcagcaacagcagacgcccaagca
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ccaaaaatgacagcgagtcgggcatcgacgaggactcccccaacagcgatgaggattgccccaatgccaacccggcgggcac atcgctcgaggacagcagctacgagcagtatcagtgcccctggaagaagatacgctatgcgcgtgagctcaagcagcgcgagt tggagcagcagcagaccaccggaggcagcaacgcgcagcagcaagtcgaggcgaagccagctgcaatacccaccagcaac atcaagcagctgcactgtgatagtcccttttcggcgcagacccacaaggaaatcgccaatctcctgcgccaacagtcccagcaac aacaggttgtggccacgcagcagcagcagcaacagcagcagcagcaccagcaccagcaacaacgaagggatagctccgaca gcaactgctcgctgatgagcaactcgagcaactccagtgcgggcaattgttgcacctgcaacgctggcgacgaccagcagctgg aggagatggacgaggcccacgattcgggctgcgacgatgaactttgcgagcagcatcaccagcgactggactcctcccaactg aattacctgtgccagaagttcgatgagaaactggacacggcgctgagcaacagcagcgccaacacggggaggaacacgccag ctgtaacagctaacgaagatgccgatggattcttccgccgctccatccagcaaaagatccagtatcgcccgtgcaccaagaatca gcagtgcagcattctgcgcatcaatcgcaatcgttgtcaatattgccgcctgaaaaagtgcattgccgtgggcatgagtcgcgatgt tctgcgcctagagcaacctaaagctggtgccaaaaataagtcatgtgaaccgagcaaaaattcgaccgtcaaccaaataaacagc aaactcgaactcggcaacagcaatgaaatgaaatga

***Drosophila* Gene Hit** TBLASTN with ORF1: ecdysone-inducible gene E75B (X51549) and nuclear receptor superfamily protein (U01087) BLASTN with genomic sequence matches ecdysone inducible gene

Annotated *Drosophila* genome genomic segment AE003522

Annotated *Drosophila* genome Complete gene candidate CG8127 Eip75B ecdysone-inducible gene E75B nuclear receptor NR1D3

Human homologue of Complete gene candidate ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA) Q15304 (9.40E-74)

Putative function Ligand-dependent nuclear receptor, putative transcription factor

Confirmation by RNAi Slightly reduced G1 and G2/M indicating fewer cycling cells

Line ID 448/23
Category Mitotic defects in brain: cytokinesis defect (very high polyploidy
Reversion NR
Map Position 75B

Rescue ID 2G4E
Rescue Sequence
GCTGGTGGACGCTGCTTTCATTCGCAAATTGCTCGTCGTTGGCAGCGGTTGTGC
AGAGCAAGAAAAGCGCGCGAAAAACCAAGCAAAAAATTAATACAGCTGGAT
CAAGCGAAAGAGATAGAGAGCAGAGTCAACAGCAACAAATGTTCAATAGCA
AATGATATCGCATATTTTTGTTGGTGCCAGTGAAGTGAGATCAAAGTGAAGTG
TGCAATGTTCCTTATTAGCAAATCGTAGAGCAACCAACAATCGAGAGTTCAAG
TGTCATTTCGAAGCCAAAAAGCAAAATCTCTAATTCAAATATGGTTTGTGCAA
TGCAAGAGGTTGCTGCTGTGCAGCATCAGCAGCAGCAACAGCAACTCCAGTT
GCCCCAGCAGCAACAGCAGCAGCAGCAGACAACACAGCAGCAACATGCAAC
AACGATAGTGCTGCTGACGGGCAATGGCGGCGGTAATCTGCACATTGTCGCCA
CACCGCAACAGCATCAGCCGATGCATCAGCTCCACCATCAGCATCAGCATCAG
CATCAGCACCAGCAGCAGGCCAAGAGCCAACAGCTGAAGCAACAACACTCGG
CGCTGGTCAAGTTGCTGGAGTCGGCGCCCATCAAGCAGCAACAGCAGACGCC
CAAGCAAATTGGTTACCTGCAGCAGCAGCAGCAGCAACCGCAACGCAAAAGA
CTGAAAAACGAAGCACAATCGTACAACAGCAACAACAAACACCTGCAACAC

Genomic hit, Accession No. CSC:AC015427
Drosophila **EST** GM03519 (A801874)

Other results same as line 343/5

Example 9 (Category 1)

Line ID	36/1
Category	Meiotic defects in testis: cytokinesis defects (Ck-04/06) `
Reversion	R
Map Position	79C

Rescue ID	A8B

Rescue Sequence
GAGTAAAGTAAACTACAGAGAAAAAACGCTTTACGGCGAGAGAACGCTTTAA
TTATACTTAATTTGTTGTTAATCAAACGCACAGAGCACACAACACAGAAACAC
AAAACACCGCTTGGGAAAAATCTGTAGGTAGANGAAAGGAGCTCACGTTTTT
CTGGTGCAGATCGAAATCGGTATCGGGTTTATTCGCTTTGCCGGATTGTTACTT
CACGTTTGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCGCACACTTTGATTT
GCGTTTGCAACTCGCAATTCGCAATTGGCATTTGCTATGCGACAACTGCCGTT
ATTTCCGGTCCGTTTACTTTTCCAATGGCTTGCCTACACACCGCCAAACTTTGG
CTTGAACTTGGGATATTGGTTGCCCGAATTTCCTGANAAATTTTTCCTT

Genomic hit, Accession No. CSC:AC013886

Associated ORF
Genscan partial ORF1: >18:33:59|GENSCAN_predicted_peptide_1|99_aa
CICFALLGLLIRRKLMVVFGSTSRKAQSLESRRAKNTSQKIGNQYPKFSQVCGKPS
KSNDRNNGSCRIANANCELRVANANQSVRRRIRNKETQLTNVK

>18:33:59|GENSCAN_predicted_CDS_1|300_bp
tgtatctgcttcgccctgcttgggctactcattcggcgaaaattaatggtggtgttcggttctacgtcgcgcaaggcacagtctctaga
gtctcgcagagctaagaatacatctcagaaaatcggcaaccaatatcccaagttcagccaagtttgcggcaagccatcgaaaagt
aacgaccgaaataacggcagttgtcgcatagcaaatgccaattgcgaattgcgagttgcaaacgcaaatcaaagtgtgcgcagg
agaataagaaacaaagaaacgcaattaacaaacgtgaagtaa

***Drosophila* Gene Hit**	rescue sequence and TBLASTN with ORF1: nucleic acid binding protein (mub) (X99340)
Human Homologue	BLASTX with nucleic acid binding protein: poly(rC)-binding protein 2 (hnRNP-E1) (S42471)
***Drosophila* EST**	several including LD32520 (AA951799 BLASTN matches nucleic acid binding protein (X99340)

Annotated *Drosophila* genome genomic segment	AE003596
Annotated *Drosophila* genome Complete gene candidate	CG7437 - mub mushroom bodies RNA binding protein
Human homologue of Complete gene candidate	4826886 ref|NP_005007.1|pPCBP2| poly(rC)-binding protein 2

	>gi|542853|pir||S42471 (4e-75)
Putative function	A putative RNA-binding protein specifically expressed in the CNS of Drosophila melanogaster
Confirmation by RNAi	Only wild type profiles observed

Line ID	472/22
Category	Female sterile (anaphase bridges, lagging chromosomes)
Reversion	?
Map Position	nd

Rescue ID sau 5'spl

Rescue Sequence

GCACGATCNCTAAAGTCTNGCANAGCTAAAAATACATCTNAGAAAATCGGCA
ACCAATATCCCAAGTTCAGCCAAGTTTGCGGTGTGTAGGCAAGCCATCGAAAA
GTAACGACCGAAATAACGGCAGTTGTCGCATAGCAAATGCCAATTGCGAATT
GCGAGTTGCAAACGCAAATCAAAGTGTGCGCAGGAGAATAAGAAACAAAGA
AACGCAATTAACAAACGTGAAGTAACAATCCGGCAAAGCGAATAAACCCGAT
ACCGATTTCGATCGGTGCGGGCCTCTTCGNTATTACGCCAGNTGGCGAAAGGG
GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACG
ACGTTGTAAAACGACGGCC
ANTGCCAAGCTCTGCTGCTCTAAACGACGCATTTCGTACTCCAAAGTACGAAT
TTTTTCCCTCAAGCTCTTATTTTCATTAAACAATGAACAGGACCTAACGCCNGT
AAC

Rescue ID Sau 5'splac

Rescue sequence

GTTGTGATCNTCTTGGTNAATCNNNTTGGAAATTCCCCTAANGCTTCCGACAA
TGACCCNGNCNTACNNAGCAAANAATNGNAGNACNNGCNGNTGGNCGTANT
ANCAANAACAGGCCCGCACCGATCGAAATNGGNATCGGNTTTATTCGCTTTGC
CGGATTGTTACTTCACGTTNGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCG
CACACTTTGATTGCGTTTGCAACTCGCAATTCGCAATTGGCATTTGCTATGCGA
CAACTGCCGTTATTTCGGTCGTTACTTTTCGATGGCTTGCCTACACACCGCAAA
CTTGGCTGAACTTGGGATATTGGTTGCCGATTTTCTGAGATGTATTCTTAGCTC
TGCGAGACTCTAGAGACTGTGC

Other results same as line 36/1

Example 10 (Category 1)

Line ID	459/2
Category	Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects: (mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05)
Reversion	NR
Map Position	66B1-6
Rescue ID	2D5P

Rescue Sequence

GCTCCGTTCGAAAGTTGAGAGAGACTTGAAACATATGTTCGGCGTTGCTAGAG
CTGGTCGGCTACCGATAGAAACATCGATAGGTCCGATGTTTTTACTCGTATAT
TGATTCANAGTTTGGCTATCGATGTTTTAGAGTGCCCGCACATTATCTATTTT
CATCTCTATTTCGTTGGTATTTTTGTATTTATGACATTTCGACTGCAAAAGC
AGGATGGCAACGCCAGATTGCCGCGAAAGTACGTTATTTTAAATTGGCGCAT
TGAATATGAAAAATTGCAGGCACATACAGTTTCTAATAAATAATAGCAATAAT
TATTATTTAGCTTGTATCATACGAAGTGCACATTACAGCTACGCATCTGAAAT
AATAATTTTAATATATCGTCTTTTCTCCCATCGATAGAGTTCCGCGCCTATCGA
TATATCGTTGATCACCAAATAAATAAAACTAAATAACGCCGCAATGGAACAC
GCGACGAGTGAATTGAGGGAATTTATCTCAGATCTTGTAATTCCGCACCACGT
TGCAATGGTAACATCAATCCGGATCACATCACAATGCTGGAAGGCACCCAGA
TCCAGAACAG

Annotated *Drosophila* genome genomic segment	AE003557
Annotated *Drosophila* genome Complete gene candidate	CG8038 - novel gene ribonuclease P homology CG7892 nmo - protein serine/threonine kinase involved in eye morphogenesis
Human homologue of Complete gene candidate	CG8038- 5e-24 4309676 gb|AAD00893| (AF001176) ribonuclease P protein subunit p29 [Homo sapiens/ CG7892- protein kinase mitogen-activated 7 (MAP kinase)' gi:4506093 and gi7706445 D919050533B3C33A |ref|NP_057315.1| nemo-like

		kinase [Homo sapiens] (3.30E-174)

Putative function CG8038: tRNA processing enzyme Ribonuclease P protein subunit
CG7892: a protein serine/threonine kinase involved in cell cycle, possibly targeted to cytoskeleton

Confirmation by RNAi Both showed a marked increase in G1 peak indicating arrest in G1

Example 11 (Category 1)

Line ID 623/8
Category Meiotic defects in testis: cytokinesis defects
Reversion ?
Map Position 37E1-3

Rescue ID 2E2E
Rescue Sequence
CTACGGGCATTCGCATGTTCGAACATCTGGTGTAAACAAGTTCTGAGCAGTGT
TGCCAACTCTTCAGTTAAACAGTTAAAAATAGCTAAAAAATGTTGACGGTAGC
TAAATTATAAAGCTAGAAAAGAAATGATATATGATAAAATAAGTATTTCGACT
CACAGCATTTATTATTTAAGACGGTCAGATGAAGTTACAAAAATCCTAAATTG
GCCCGCTGTATCTAAGAATTAATACCAAGAAGTTGTCATCAAAGGTCGAACTC
GACGGAAATTCTACTTTGAGTTTTTAAATTTAATAAATATGTATTTAAAATTAT
GTAAATTTGTTTGTAAAACAAAAATAGTATATAGTATAGTAATAGTAGTTAAG
TAGTTTTAAAAATGGCCAGATCAAAGACTTTTGAGATATGATACTAATCAAAA
GTCGAATTCGCGGAATTAATTCTTGAAGACGAAAGGCCTCGTGATCGCCTATT
TTTATAGGTAATGTCATGATAATAATGGTTTCTTAGACGCAGGTGGACTTTTCG
GGGAAATGTGCGCGGAACCCCTATTTGTTATTTCTAAATACATTCAAATATGT
ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGG
AAGAGTATGAGTATTCAACATTTCCGGGCGCCTTATTCCTTTTTTGGGCGGCAT
TTGCCTTCCTGTTTTTGTTACCCAGAACGCTGGTGAAAGAAAAGATCTGAAGA
CAGT

Annotated *Drosophila* genome genomic segment AE003662
Annotated *Drosophila* genome Complete gene candidate CG17559 dnt - doughnut protein tyrosine kinase

Human homologue of Complete gene candidate Homo sapiens RYKreceptor tyrosine kinase GDB:21773

Putative function growth factor transmembrane receptor protein tyrosine kinase involved in cell growth and maintenance

Confirmation by RNAi Only wild type profiles observed

Example 12 (Category 1)

Line ID	629/14
Category	Meiotic defects in testis: cytokinesis defects (Ck-06/09)
Reversion	NR
Map Position	64D

Rescue ID 2A9X

Rescue Sequence 1

GACGGGAGGAAGTAAGTGGGAGGAGAGAGTAGTGCCTCTTTTTACTGGAGA
AATGGACAAACTCTGGGAACTGCGAACTGCGAACTAACCGAGGCAAAAATTG
AGAAGCGAGCTGAAAGCGGAATTCAAACAACGCAGCGCTGACGGCGACGCCG
GCAGAAGCAGCGCCGCACAAGGCATGCGCACAGAGAGTAAGAAAGAGCGCG
GCTAATGAATGAATGAACGAGGCGGAATGCGGGAAGAGCGCAGAGAGGCGC
AATGACAAAATAGTTGTAGAAAAGCGCCGGCAAGCGGAACTCCACACTCTTT
CTCACTCTCTCTTTCCACCCACACCCCTAGTTCACCGGAAAAAGAAAATTCGTT
TGCGGCGGGGGTGTATTTTTCACCAAAAAGAGAGTGTGTGCAAAACGCTAGA
GAGAGAGAGAGAGAGAGAAAGAACTGACGTCAGTTCTGCCTCCGTCGACGCC
GCTGCCGGCGTCCCAAAGCGCCACCACCCAAAAAAACGCGAGAAGAAGCAGA
ACAAACACACACAAAAATTCGCACAGTGGAGCAGAAATCAAGC

Rescue ID 2A9E

Rescue Sequence 2

CTCCCGTCGTTTTGAGATCAGCTGCTCTCGCAACAACAACAACTATAACTGTA
GTTACCGTCTCTTTTGCATCGTTCGTTTTTCGTTTGTGTCGCCAAGTGATTGTGT
GTGTGCGTAAGCTTAAAGCTGACTAACAAAACGAAACAAGAAAAAATATAAA
TTATAGGAAAATTGTTAAATTATAACCAGAAAGAGAGCGGCACTTACGTGTGT
TATTGTGTGCGTGTGCTTTAAAAAGATATAAAAATAGCAATAGAAAGTTATTA
AAGCGTTGGCAAAAAAGTCCAACGAACAGCGAGAGGAAGCGGAGAACGAAA
TAGTTAAAGCCAAAGTCGCTGCCGACGTCGCACTTGAAAACGTCGCAAAAGTT
TGTAAACACACCAGTGTGTGTTCGTGTGTGTTTTTGCCGGCGTGCCAGTGTGCG
TGCGCCTAGAAAAGAGTAAAGAAGCAGAAGAAAAGGAAGAAGCCGAAGAAG
CAGCAAAAGAAGCCGACAGCAAAAAGTAAATAAAATCAAATGCCCCCTGGCA
GAATAATATTAAATTAAGACACATACTCAAATTAATAAC

Genomic hit, Accession No. CSC:AC015076

***Drosophila* EST** LP08767 (AI295205)

Annotated *Drosophila* genome genomic segment	AE003567
Annotated *Drosophila* genome Complete gene candidate	CG10668 - novel with homology to ssDNA/RNA binding proteins
Human homologue of Complete gene candidate	CG10668 - 3e-12 4506449

ref|NP_002889.1|pRBMS2| RNA binding motif, single stranded interacting protein 2 >gi|1082

Putative function Possible single stranded DNA/RNA binding protein

Confirmation by RNAi Slightly increased G1 and reduced G2/M indicating G1 arrest

Example 13 (Category 1)

Line ID 653/12
Category Meiotic defects in testis: segregation defects, cytokinesis defect (Ck-07/35)
Reversion NR
Map Position 75B

Rescue ID I5E
Rescue Sequence
GTAAAAGCTTAGCCCATGGCGTCGACGTCGACTGCGACAGCGACGCTAGCCG
AGGCAGTGACTGCGACGTTGGCCACTTTTCGCCTTCGTTTCGCTGTCGTTTTCA
GTTGTCTCTCGTTGCTCAAAGCGCGCGGCACGCGAACGCTCTGAAATCCCAAG
TTACAACAGCAACATCAAGCAGCAGCAACAACAGTGATTCGCTGGCAAACAA
ACAAACAAACCAACATATTTTTGTGTATCAATTGTCGGCCTAAAACTTCACAT
AAAAGTGCGTTCAATACGAAACAAATATATTTGTATATATAGAGAGCGAAGC
AATCGGTTGCATAAATTGAATTCCGTTCATATACTTCAATATAAATATTATTAA
GTACTACAATTTGAAAACATCTTTAAATATACAACATATTTTGAATTAAGTTTA
TTTTTTTTTTTAGCCACATAGAGACATCTTTGTGGCATGCTAAATTCTGTAGTA
AAACTTTCTTGGGGAAAGTGAAAGCCACGTATCAGACCAAAATCCACCCAAC
CCTGCACACACGCATCCCCATAAAGAACGACCTTGAGCT

Genomic hit, Accession No. CSC:AC014071

Associated ORF
Genscan ORF1 predicted sequences >16:36:33|GENSCAN_predicted_peptide_2|477_aa
MLILMRPSIKLAANQNAIKAPNGPKNFLDKVLVVRCWLSVCLLENGHIAVTASGS
NNNNNSNNINLNLKANYQMSATSIRDSFATILLDAQNRVQNATVAAKNFMLPLR
LRSDTSGDTSNNNENNSRRARQAYNCGVNWLTTHRPKRRRQVHPPLGSTPSCNN
NSSKISRNSSSSSNNIASATATRIFLGTSAILAIDFDNTRVPGYYQPTGEWIWVSKS
MIKQLFAVAATADDVAAAAASRGNALTFLPGKEKGPRKKAEGCGMEWSGVEWS
GGDVMCVLSSVATVDDDDHHGGGHFDGLLGTPSALIRLNCLINPKKMRMDFEVE
VAWQIARAADLRLISMHLNVPYEMKTMKTMESVIDGGSLYQPTALFGSLFCLVY
SSAADVLLLLANCKSLAHGVDVDCDSDASRGSDCDVGHFSPSFRCRFQLSLVAQS
ARHANALKSQVTTATSSSSNNSDSLANKQTNQHIFVYQLSA

>16:36:33|GENSCAN_predicted_CDS_2|1434_bp
atgttgatcctaatgcggccgtcaatcaaattggccgcaaatcaaaatgcaattaaagcgccaaacgggccgaagaactttttgga
caaagttctggttgtccgctgttggctgtctgtctgtctgcttgagaatgggcacattgctgtcactgccagcggcagcaacaacaa
caacaacagcaacaacatcaacctcaatttgaaagccaactatcaaatgtcagctacaagcatccgagattcgttcgccacgattct
tctagacgcccaaaatcgagtgcaaaacgcaactgttgctgccaaaaacttcatgttgccgctgcgcctgcgcagtgacaccagc
ggtgacaccagcaacaacaacgaaaacaacagccggagagcaaggcaggcttataattgtggcgttaactggttgacaacgcat
cgcccgaagcggcggcggcaagtgcacccgcctttgggttcaacgcccagctgcaacaacaacagcagtaaaatcagcagaa
acagcagcagcagcagcaacaacatcgcatcagcaacagcaacacgcatttttcttggcacttccgcgattctggccatcgacttc
gacaatacacgagtaccggggtattatcagccaactggggagtggatttgggtatccaagtccatgattaagcagctgtttgctgtt
gctgccactgcggatgatgttgctgctgctgcagcttcacgcggcaatgcgttgacctttttgccgggaaaggaaaaggggccaa

ggaaaaaggcggaagggtgtggaatggagtggagtggagtggagtggagtggtggcgatgtgatgtgtgtgctctcgagtgtg
gccacagttgacgatgatgatcatcatggtggcggccactttgacggcttgttgggaacaccttcagcgctcatccgacttaactgc
ttaatcaacccgaagaagatgaggatggactttgaggttgaggttgcatggcaaattgctcgagctgctgatctgcggctgatctca
atgcaccttaatgtgccttatgaaatgaaaacgatgaagacgatggagagcgtgatcgatggtggctccctgtaccaaccgactgc
tctcttcggttctttgttttgcttggtgtattcttcagctgctgatgtgttgttgctgctggcgaactgtaaaagcttagcccatggcgtcg
acgtcgactgcgacagcgacgctagccgaggcagtgactgcgacgttggccacttttcgccttcgtttcgctgtcgttttcagttgtc
tctcgttgctcaaagcgcgcggcacgcgaacgctctgaaatcccaagttacaacagcaacatcaagcagcagcaacaacagtga
ttcgctggcaaacaaacaaacaaaccaacatatttttgtgtatcaattgtcggcctaa

***Drosophila* Gene Hit**	rescue sequence, ORF1 and genomic sequence: Canton S E78B nuclear receptor superfamily protein (U01088)
***Drosophila* EST**	LP11082 (AI296953 similar by BLASTN to U01088)

Annotated *Drosophila* genome genomic segment	AE003593
Annotated *Drosophila* genome Complete gene candidate	CG18023 - Eip78C Ecdysone-induced protein 78C nuclear receptor NR1E1
Human homologue of Complete gene candidate	CG18023- 4e-32 119100 P20393 EAR1_HUMAN V-ERBA RELATED PROTEIN EAR-1 >gi|1082832|pir||A32608

Putative function	ligand-dependent nuclear receptor , putative transcription factor
Confirmation by RNAi	Not done due to failure of PCR procedure

Example 14 (Category 1)

Line ID 876/2
Category Meiotic defects in testis: cytokinesis defects
Reversion ?
Map Position 73A

Rescue ID 2H1E
Rescue Sequence
GATCAAACAGAAAATCCAAAAACGAACAGCGCGCGGCGAACGAGAGCCGTT
GAAGCCGGCAGAGAAGTGCGCTGCTCGCGTCGCTGCCGGTATGTGCGTGTCTG
TGCACTGAGAGAAAATGCTCGATTAAACAGAGAAATTAATAGTAATATAAAA
AAAAAAAAAATTTGTTTATTATTCTCAATTCAATAAAATGTAATTATTTATTAT
ATTGGTTGTATAAGAATTTTTATAAAGTAGTATAAATTTTCAATCAAATAAAT
ATGTACATCTAACAAAAAATGTTATTATCTTATAACAAAGAGGTAAAATCATA
AGTAGTACGAAATCTTTAAAAGAGAAAGTGTGTTACGCAAAAAGTATTCAAA
GCAGTCTTTTATTTAATTTAATTAATTTATTTGTGCTTTATCCCTTATATATATA
TGTACATTTCATTAAAGCTAATGGTATAATTAGGTATTTACAGTGTTTAGCTAA
GGCTTTCATCTGAAATATTTATTAATTATGTCTAGTTGACCTGTTTTTAGTTTTT
TTGNATAACAATATTTATTATTTATTAAGGAAAACAAGGGGAGAAGAAAAAC
CTTAATTGAAGCAAAGCAGTCTTTTGAACCCACTGGTG

Genomic hit, Accession No. AC005633
***Drosophila* Gene Hit** rescue sequence: argos (M91381

Annotated *Drosophila* genome genomic segment AE003527
Annotated *Drosophila* genome Complete gene candidate CG10162 – Egf2 translation facto

Human homologue of Complete gene candidate CG10162 - 4e-11 181969 (M19997) elongation factor 2 [Homo sapiens]

Putative function Translation elongation factor

Confirmation by RNAi Not done due to failure of PCR procedure

CATEGORY 2: FAILURE TO ENTER M-PHASE

Example 15 (Category 2)

Line ID 1216/12
Category Meiotic defects in testis: no division (no meiosis)
Reversion NR
Map Position 82F1-2

Rescue ID 2I5X-1
Rescue Sequence 1
AAACCAAGCAACAGAAATATCTCCAGTAGAGAGCGCCACTGGAAGATCGGAA
TTTTTAGTGCTCTGCTCTGACTAACAGGTTTTAGTAGTAGTGCTTACTTTTCTAC
TACGATTTTTGTCGCGGCTAACAATTCTGTTTTCCCACTCCCTCTCTCAGTTTTT
GCATGGTAACTTTTCGGTCATTGTACTGTTGTTGTTGTCTTGCACACCGCAAGA
GAACAACAACAATCGGAGAAACACTGATAGCGCGGTACAGTGGGGCAGGCCA
AACTAGAACCTATACATTTAAGATGTCTCCAATTTGTGATTTTGCCTTTCAAGC
ATACTAGTTCATAGTTGATTGTTTTGTTATGTTTTGTCTTGAATGCGATGTTTCA
AGAAATCTTATTTTCGAATTACGATATTATTCTTATTCCTTTGACTTATTAAAA
TAAATGAAAACGGCGAGTAGAGCAAAAGAGCGACCACTGTGGCTCCACAAGC
TCGTTTCTCTGTTTCTCATTCGCGCCAGCTCCAATTTCGCCTTATTCACACACA
CACCTCACTGCTTGCGACTGCAAATTTGTGCAGCTGAACTTTG

Rescue ID 2I5E-1
Rescue Sequence 2
CTTGGTTTATCACCCTCTCTCTCTCTCTATCGCGCGCGCGCTCTTTGTGGAA
ACAGGTATAACTGTTTGGCGTGAGGGAGCACGAAACTCCAGTGGAGACTTCTC
CGCATCGCCAGCGAAACAAACGATCAAAATGAATACTCTGATAACGTGTGAA
GGTGAGCAACAAAATAAAGTATAAGAAAATACCGCCACGAAAACAACAACA
ATAGAAATGTCGACGCACCCTTTTCTTTTTCTCGCAAAGAACGAGGAAATGGA
GAAGCGCAAAACCACATCCCGCTTAAAGAGTCCCTTTCCCCCGCTGGAAGTGG
AAGGAAAGGCAGCTTAAAGAGGAGCGGGTGGCTTCCAGTATGTGGAAAACAA
AGCAGACGCCATTGGAATGCCGTCGTTTTTTGTTGTTGCTAAGCCGGACATGG
CAATTGTTGCTTTTGTTTTCGAGAGGGGGTGGTGAAACTCATAAATATCAGCT
ATGGCGAGGGGGTGGGGGCAGTCTTTGTCTGACGTACCGTACTTTTAATTTCTT
GTCGCCCGGTTTAATCCAATTTATCCAGCTTTGAATTTCGCGG

Genomic hit, Accession No. AC007532

Annotated *Drosophila* genome genomic segment AE003603
Annotated *Drosophila* genome Complete gene candidate CG1116 - novel

Human homologue of Complete gene candidate 2495728 HYPOTHETICAL PROTEIN KIAA0258(aa)

Putative function No homologies which indicate function

Confirmation by RNAi Slight loss of G1 peak

Example 16 (Category 2)

Line ID	1344/15
Category	Mitotic defects in brain: no mitosis
Reversion	NR
Map Position	83C

Rescue ID 2F6E

Rescue Sequence

AGCGGGAGTGAGCCGAAAGAGAGTAATTTTGGCCGTCACCAAAAAAGTGGCT
GCATAGTGCCAAACCAATGTATGGCCGTTACGCATCTTGTTATTCTAGTGTCTT
TGGCTGTAATCAGTTTGCAGTGACAGAGGAGTTCAGTTTCAGTTGACTCGGCT
TGGTTCAGGGTTTCTGATTGCCGTCCTCTTCTCCCTCTTCGCCTACAAGTCCGC
TGTTCGGCACCGTGACGTCACCTAGACTTACACCCCTAATCAAAGATCCACTA
GTTTAGATTTCCTGCATCAACGCCATATTAACTTTATAAGCAGTCGTTATATCT
CAAGTAGGCAAAAAAGTGTAATAGATATGTATCTAAATTGTCGTACATTCTAT
TTATTAAAATTCGTTTTTACATCCAACAGGTGTTATTTTGAAGTCTTAGATAA
CAAACAATATTCGAATTATGTGGTAGAATACTTAGCAATATACGCACATACAT
ATACATATGAACATTATATCCAATGCTTTAAAACCGGAATATCAAGACAACAT
AATGCAACATCTGGTCCGAGCTATCCAGGCAATCACATTTTTGAAGTTCCCCC
GGTTATCACACATATATCGATCATACCCCGAAATGTGTAACACAGATACAGCT
CACCATCCCTCTGATAAGATCTTATCAAGTTCGGGCTTGCTCGCTATCGTGAAT
TGGGTTGAAGGGTCCGCGATAATTGCATTGGGCATGCCATTGGTAATCACAAT
TGGCTGATAATGCTGCTGCTGCAATTCCACGGGTATGAA
TTCATCAATTGGTTA

Annotated *Drosophila* genome genomic segment	AE003602
Annotated *Drosophila* genome Complete gene candidate	CG1347 - novel protein with myosin homology
Human homologue of Complete gene candidate	1503990 |dbj|BAA13194| (D86958) KIAA0203 similar to mouse CC1.(aa)

Putative function similar to coiled coil protein with ubiquitin like domain

Confirmation by RNAi Marked reduction of G1 and G2/M indicating fewer cycling cells

Example 17 (Category 2)

Line ID 703/16
Category Meiotic defects in testis: segregation defects, meiotic failure (Mf-07/75)
Reversion R
Map Position 83B

Rescue ID 2E7E
Rescue Sequence
AAGCAGCCCAACAGCTACGCAAAAAGTTACTTATATTCGCAGCAAAACAGAT
TTTTTTGTTTTAATCGTAAGTATAGGAGTGAAAAATAGCGCTAGAGTAGACCT
AAGTACACAGAAAGACAAATAGGGCGAGTAAAATCGCGGTCCTGGTCATTTC
TCTGGCCTTGACCAATCCTTTGTCTGCGCTTTCGTTGGAAAAGGGGTTATGTAC
GAACTGCGTGCGTACCTAAGGCCAGATTAGTCATCGGGCAGTCATATATTCAT
GCAAAAAATCATTTGGTGGCCGTCGGCCTTTGTTCGACTGTACCTTGCTCATTA
TTTAATAAGCGCGACAGCAATATACACACTTTGAACCCCCATCCCACATTTTTT
CTCACCGTTTCCCCCTAATTTTCGTTTTCCCTGTGCCCATCATTCCGCTTTCGCC
ATGTCAGTGTATCGCTTCAAAATGGCGCCGAACCACATGTCTTCGTTCTCGGC
TCGTCCGCTTCGTTCGTGCGCTCGTGTGTCGTCTCATTCGCTCTCCGAATTTCG
TTTAACAAAGTGGTGCGAGCAGAGGGGCCGCTGGATTCGAGGCAAACAACAC
ATATACCTA

Genomic hit, Accession No. CSC:AC013960

***Drosophila* EST** several including LD15903 (AA440858), GH20091 (AI389018).

Annotated *Drosophila* genome genomic segment AE003602
Annotated *Drosophila* genome Complete gene candidate CG2922 – novel

Human homologue of Complete gene candidate 286001 dbj|BAA02795| (D13630) KIAA0005 [Homo sapiens] also NP_054757.1| HSPC028 protein [Homo sapiens] e-179

Putative function Weakly similar to a region of human and murine EIF4G2 translation initiation factors; may act as a translation initiation factor

Confirmation by RNAi Only wild type profiles observed

Example 18 (Category 2)

Line ID	741/3
Category	Meiotic defects in testis: segregation defects, meiotic failure (Mf-05/31)
Reversion	NR
Map Position	88D

Rescue ID H6E

Rescue Sequence

GCCTGGAGCCACCTCTAGAGCCACGGCCAAAAAATTGTGTGCCAAAAAATCG
TATGGCGTTACGCATCTTGTTATTCTAGTGTCTTTGGTTCTACAAATCTGGCCA
ATGGGATGGACGGATTTTGGGGCTTTTGCGCCCCACATATGTNTCTTACAACC
CACTCGGCCCGGCAAGTGGGTGTCAATTACGGACATCGGCAATCCGAAGACC
GGAGACCCAGAGACCCTCAGACCCCAGGGCCCCATTCGATTCGATTTCGAGTT
GCGTGGGCCGATCTCACATTAGTCACATCGAAGGAATGAAATAAAAAGAAAA
AACATGACGGCCGAAAAGAACTTATCCATCTTCAAAGCTCTCAGAAAATACA
AAAAACTAAAAAACTTTTGACTCTTCGTCTTTCACATTTCGAAATCACAAAAT
GTCTGCCATAAATTCCAAAGTGAACAATTGAAATAAATTTTTGCGCCATGAAC
ACGCCGACTG

Annotated *Drosophila* genome genomic segment AE003705
Annotated *Drosophila* genome Complete gene candidate CG12600 - novel protein

Human homologue of Complete gene candidate CG12600- 5e-27 4240227 dbj|BAA74892.1| (AB020676) KIAA0869 protein [Homo sapiens]

Putative function putative cytoskeletal structural protein

Confirmation by RNAi Reduction of G1 and G2/M peaks indicating fewer cycling cells

Example 19 (Category 2)

Line ID 773/1
Category Meiotic defects in testis: cytokinesis defects, meiotic failure (Mf-02/15)
Reversion R?
Map Position 83F

Rescue ID 2D9P
Rescue Sequence
CCACCGCCCATGCCGCCATTTATTGAAAGGCCTGTACGCAGTTTGTTTTGTTT
TTCTCTTTTTTGCTAGCTCAAACACAAAATTACTTTTTGTGGCTTGACTGGTGA
GGTCTCTCTATCTCGCTTTTTCGTCTTTACCTCGCTCTCATTCCCTCTCTATCTG
CCCTGCTTCCTCTCACTATCTATCTACAACTGAGGTCAACAAAATAAGTGCGT
AGTCAAAAATGTAATTGAATTGATTGACAAACACAGCGAACGTAAATTTCCGT
AATGTTTAACCTTGAATTCAAATGAACAACTGTATAAATATAATACACGGGTT
AAACTCCATTTCAAAGCAAGCTAAAACATTTTAAATACATTTTAGGGAAACGG
CCAATTAAAAGAATAATATTGTGGGGATCAATCTGGGGAAAAATGCAGTATC
AGTAATGCTGAATATTTATTTACTAAATTACAATGAAATGTCTCAAACAAAT
GGGTTAATCATTTTCTTGCTCCATCTGCTTTTCCCAACTGTATCCAAGTACAAC
TACAGCATTATCCTCAACTG

Annotated *Drosophila* genome genomic segment AE003675
Annotated *Drosophila* genome Complete gene candidate CG10272 - novel protein

Human homologue of Complete gene candidate CG10272 - 2995577 AC004490 (AC004490) R29381_1(aa) protein includes HMG-I and HMG-Y DNA-binding domain (A+T-hook) found in HMG non-histone components in chromatin

Putative function Chromosomal protein

Confirmation by RNAi Loss of G1 peak indicating arrest in G2/M

CATEGORY 3: METAPHASE ARREST

Example 20 (Category 3)

Line ID	1067/13
Category	Mitotic defects in brain: prometaphase arrest (overcondensation, polyploidy, scattered chromosomes with bipolar spindle)
Reversion	NR
Map Position	69C4-10

Rescue ID 2F8E

Rescue Sequence

GTTTGGGCACAGGGTTGTATTTCATTTATTTTTGGGGGGAGTCGATACGCTCTC
TTGGCGTGGTCGAACGGTCACACTGGCCGAGAGATAACGGAAAATGTTTCAA
AGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACTATAATTAGCTTACTA
TTCCAAGTATGTATAATTATTACACGTTTAAAAGGCATAACGTTAAGTGTAAC
CAAATTATATCAATGGATTTTGAATACCAATATTATTTATTTTATATTTTGAGC
TTAATATATTAAATCACATATATTTAAGCCTCTTTATATATGTAAATATTTTAA
TTTTATTAAAATAAATTATATATTGTTTTGTAATATGATCGAGGGCTGCCACCT
TGTGATAAATGCTTACCAACACTTTTAGGTACGCCGTTTAGTGTACGTAAGTTG
CGTACCTAGATATCCAGCGAAATCAAAACATTGAGTAAATCGTGGAAAATGG
ATGAAAATAGCTTAATCTACGGACTCGAACTGCAGGCGCGGGCTTTAACACCT
CAGTACGGAGAGAGCAACGATGTGTGCTTCTTCATAGCCACCAACTCCTTGAA
GCCCACCAATCAGGTTCACTTAATCCAGTACGAAGA

Genomic hit, Accession No. CSC:AC020333

Associated ORF

Genscan: ORF1 predicted sequences: >16:51:11|GENSCAN_predicted_peptide_2|178_aa
MAQNISPEQSGGAGGGGSKHSDDSMPVKDNHAVSKRLHKELMNLMMANERGIS
AFPDGENIFKWVGTIAGPRNTVYSGQTYRLSLDFPNSYPYAAPVVKFLTSCFHPNV
DLQGAICLDILKDKWSALYDVRTILLSIQSLLGEPNNESPLNAQAAMMWNDQKEY
KKYLDAFYEKHKDT

>16:51:11|GENSCAN_predicted_CDS_2|537_bp
atggcgcagaatatcagccccgagcaaagtggtggagcaggcggcggcggcagcaagcacagcgatgactccatgcccgtg
aaagacaatcacgccgtgagcaaaagactgcacaaggaactgatgaacctgatgatggccaacgagaggggcatctcagcgtt
tccggacggcgagaacatcttcaagtgggtgggcaccatagcgggtccacggaacacggtgtattcggggcaaacgtatcgttt
gtcactggattttcccaattcctatccgtatgcagcacccgtggtgaagttcctgacgtcctgcttccatcccaatgttgatctgcagg
gcgccatctgtttggacatactgaaggacaaatggtcggccctgtacgatgtgcgcaccattctgctgtccatacaatccctgctgg
gcgaaccgaacaacgagagtccactgaatgcgcaggccgcgatgatgtggaatgac

***Drosophila* Gene Hit**	TBLASTX with ORF1: poor homology to several sequences including homolog of RAD6 (DHR6) (M63792), bendless (L20126) and Ubc D1 mRNA for ubiquitin-conjugating enzyme (X62575).
Human Homologue	TBLASTX with ORF1: ubiquitin carrier protein E2-C (UBCH10) (NM_007019.1) and ubiquitin-conjugating enzyme E2B (RAD6 homolog) (NM_003337.1).

Annotated *Drosophila* genome genomic segment	AE003541
Annotated *Drosophila* genome Complete gene candidate	CG10682 – vihar ubiquitin-conjugating enzyme
Human homologue of Complete gene candidate	gi5902146 0B6F58A1F0665D9A |ref|NP_008950.1| ubiquitin carrier protein E2-C [Homo sapiens] (2.50E-50)

Putative function	Cyclin specific ubiquitin conjugating enzyme
Confirmation by RNAi	Complete loss of G1 and G2/M peaks indicating fewer cycling cells. Immunostaining shows metaphase arrest with condensed chromosomes

Line ID 1105/1
Category Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest
(Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle)
Reversion R
Map Position 69C

Rescue ID A5B
Rescue Sequence
GTACATATAATCACAATTGAGAATCGAAAACCCGACCGCCACGAAGCGCGCT
AAATTACACGCACATACTGAAAGCCAAACAGCGGATAGCACTAGCATCCTAC
ATATATAGACGTAGATATATAGTCATGGCGCAGAATATCAGCCCCGAGCAAA
GTGGTGGAGCAGGCGGCGGCGGCAGCAAGCACAGCGATGACTCCATGCCCGT
GAAAGACAATCACGCCGTGGAGCAAAAGGTGAGTATCACATGGTGCAGCCTA
AGATAATCCGCCAATATACACACACACTCACACTCACCCACAGACTGCACAA
GGGAACTGATGAACCTGAATGAATGGGCCCACCGAAAAAAGGGG

Rescue ID A5E
Rescue Sequence 2
ATATGTACTGTATAGTGGAAATTTAGTTTGATCGGTCGGAATACGCGTCTGTT
GCTTTTTCAGATATTTTTTTTTTCACTTTTGTGTGAAAACAAAATGGAAGGAGA
ACGAGAAGAAACTGTGTTTGGGCACAGGGTTGTATTTCATTTATTTTTGGGGG
GAGTCGATACGCTCTCTTGGCGTGGTCGAACGGTCACACTGGCCGAGAGATAA
CGGAAAATGTTTCAAAGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACT
ATAATTAGCTTACTATTCCAAGTATGTTATAATTATTACACGTTTTAAAAGGCA
TAACCGTTAAGTTGTTAACCCAAATTATATCAATGGATTTTGAATACCAATATT
ATTTATTTTATATTTTGAGCTTAATATATTAAATCCACATATATTTAACCCCCCT
TTATATATGTTAAATATTTTAATTTTATTAAAATAAATTATATATTGTTTGGTTA
AAA

Genomic hit, Accession No. AC007328 69B-69C

Associated ORF
Genscan: ORF1 predicted sequences
>/tmp/aaaaanjda|GENSCAN_predicted_peptide_1|357_aa
MGKKAKHKKKGKGPEKTAMKADKKQAARQKKMLEKLGEANIADIIQLLEAKEG
KIEAISESVCPPPTPRSNFTLVCHPEKEELIMFGGELYTGTKTTVYNDLFFYNTKTV
EWRQLKSPSGPTPRSGHQMVAVASNGGELWFPNFACISRNQSWFVFHNCRLKAA
SREKVLLNFNGTVLHPANNIIVHVKLFKKANGFKPWLLDVKLDACRFVRTNFHPF
VRIIFDLFKDFSTINHTCPYVVLRSMRYIVRRSPRLVHPIVDVPAIGHTRPRRKAAV
RGIGCAHRCPLIRMATPCRTNVVMMTLMRGSVRSRVMAICCYRRPAIAIARRRHP
TAIAHSQEVAERLGGLLYPDIQRTNP

>/tmp/aaaaanjda|GENSCAN_predicted_CDS_1|1074_bp
atgggcaaaaaggccaaacacaagaagaagggcaaagggcccgagaaaacggccatgaaagcggacaaaaagcaggcgg
cgcggcaaaagaaaatgctggaaaaactgggagaagcaaatatagctgatatcatccaattgctggaggccaaggagggcaag
attgaagccatcagtgaatccgtttgcccgccaccaactccacgatccaatttcaccttagtttgccatccggaaaaggaggagctc

atcatgtttggcggcgaactgtacactggcacaaaaaccacagtgtataacgatttgttcttttacaacaccaaaaccgtcgagtgg
aggcagctgaaatcgccatcgggacccacgcccagaagtggacaccaaatggtggctgtggccagcaatggaggagaactct
ggtttccgaacttcgcctgtataagtcgcaatcaatcctggtttgtgttccacaattgtcgtctgaaggcggccagtcgtgagaaggt
cttactcaactttaatggaacggttctacatccggccaataacataatagttcacgtcaagctgtttaaaaaggccaacggttttaagc
cttggttattagacgtaaaactcgatgcttgtcgctttgtgcggaccaacttccatccgtttgtacgcattatattcgatctcttcaaagat
ttctccaccataaaccacacgtgcccatatgtggtcctccgatcgatgcggtatattgtccgccgatccccacgacttgtgcacccc
atcgtagatgttccggctattgggcacactcgccctcgacggaaggccgccgttcgtggcatagggtgtgctcatcgctgccctct
gattcggatggcgactccgtgtcgtaccaacgtggtgatgatgacgctgatgaggggctcggtgagatcgagggtgatggcgatt
tgctgctaccgccgacccgccattgccatagcccgtcggcgccaccccactgccattgcccactcccaagaagttgctgaacgc
ctcggtggtcttctttacccggacattcagagaaccaatccgtag

***Drosophila* EST** several ESTs including LD04777 (AA201675)

All other entries as for 1067/13.

Example 21 (Category 3)

Line ID	1407/13
Category	Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle)
Reversion	NR
Map Position	92B1-3

Rescue ID 2D3P
Rescue Sequence 1
ATCACGAATTTGACATTGCTACCACATTCGGTGCGTGGACTCTGAAAGCTCTG
AGTGTTTTGTTTATGCAAAGCTTTTTGGACTATCGCGTGGTAAGTAGCCGAAA
GAGAAAGCTCTCTTATACGGAAGATGAAGAGTGTGATTCATGAAAATGTATA
AGAACGCGGGTCCAAAAAGTCAAGGGAGTTCTAGTGAAATGAAAAGTTCCAA
AGGTTTTGAAATCGTTTTATTTTCTCGTTCGTATAATTATTGGGTGTCGATCTTT
GTTGGGCAGTGTAAAGCACAAACTTTGAGCTTCATCATACATATCATATGTAA
AGCCGGGACGAAAGCTTATGATTCTGTTAAGTGTCCGCCCAAGATAACATTTC
TCCAGCCCTTCAAATCTTCAAATAAATACGGCTTAAGGCGAGCAAATTTGTAA
ATCAAATGATTTGTTAAATAAACATTATATGTATTTTATCATGCCAGGTTAGAA
CACATTGTGCTGATGCAAATAAAATTCCAATTAAACGCCCCTGAATGGGAAGA
TGACGCATCTTTAATGGGAATATTATGGTAAATTTAATA

Rescue ID 2D3E
Rescue Sequence 2
TNCGTGATTATCAGCGTTAATTGTACAATATTATGATTTATTCGAGCTGTAAAT
CTTCACAGCAAGCACAAACTGTAATTATACCACTTAGAATTCCGCGGAATTAA
TTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCAT
GATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCG
GAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA
GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAG
TATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCT
GTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTG
GGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAG

***Drosophila* EST** LD05707 (AA246767)

Annotated *Drosophila* genome genomic segment AE003727

Annotated *Drosophila* genome Complete gene candidate CG7444 - very short ORF with EF hand homology

Human homologue of Complete gene candidate none

Putative function Possible calcium binding protein

Confirmation by RNAi Slight loss of G1 peak

Example 22 (Category 3)

Line ID	1439/7
Category	Mitotic defects in brain: prometaphase arrest. (overcondensation, polyploid, no anaphases, scattered chromosomes with bipolar spindles)
Reversion	?
Map Position	96F10-14

Rescue ID G3X

Rescue Sequence

GTCGGATGTAGAAGACGTGCCCGAAACCCAGTTAGAAATCGATGTCAGCGAT
GGCGCCGGACTGGAGGATGAGGATGATGACGATATGGAACAGATTACAGCTC
AGAAGGTAAGGTAAATCGTAACAGAGCTTTTTAATACGCAAGTAATCACATTC
TGATATCCCTAGGTTCTGGAAATCATAGAAACCGCGTGGATAAATGAAATGTG
TGCGCCGGAGATCCTGCCCAGCCAGACGGACATGCTGGAGCTGATGGTCTCCC
AGGTGGCCCATATGGAGGAGCAGATGCGCGATCTGGACAAGAACGATTTCCG
AGCGGTGGTGCACTCCATGGAACTGGAGAGGGTGCGCTACATAATGGCCAGT
TATCTGCGTTGCCGCCTGCAGAAGATCGAAACCTTCACGCAGCACATCCTCAA
CCAGGAGGAGAGCCGTGAGCCGGATGACAAACGTCTGTCTCCCGAGGAGACT
AAGTTCGCCCAGGAGTTTGCCAGTAAT

Genomic hit, Accession No. AC007825

Annotated *Drosophila* genome genomic segment AE003754
Annotated *Drosophila* genome Complete gene candidate CG14549 – novel

Human homologue of Complete gene candidate none

Putative function no homologies which indicate function

Confirmation by RNAi Only wild type profile observed

Example 23 (Category 3)

Line ID	1466/4
Category	Mitotic defects in brain: metaphase arrest. (overcondensation, no polyploidy, fewer anaphases, metaphase with bipolar spindle)
Reversion	NR
Map Position	72F

Rescue ID E5E
Rescue Sequence 1
GGCTGGATGCGATTCGCTTTCGGATTCGGATGGATTCAGCCGCTGTCTCGACA
CCGCCGCAACCGCTCTCGGGAGTTTGAAAATTTGAAATGAGCGGATTCGCGTT
GCGAAGGCGAGCTAGCGTTGCAGGCAGTGTGGCCAGATGCCGCGTGCGAACG
TATTCTCGAATGCAATCGGCCGAGTGCAGATGCACTAAAAATAACCCACTTCC
AGTGACTGGAAATTAAGATCAAGGNAATAGATTTTATAAAAACTTATATGAGT
AAAAATTTTAAAATTGTGGAGTCAACCTAAATTATAAGCAACTAATTTATAAC
ACAAGTAAAGAATGATATTAAGTAACTTTTTAAATAATATTCCATTATGCTTA
CGCTCAATTTATGAACAAATGTTTTCTCGATCCTTAGGTAAAGTTTCGAGTTTC
GCGACTANATTTATTAAAATTAAGAACATCTCCATTTATGTACACATTTAAAG
ATTTATGAGCGGTAATATTAGCTGGTTGAC

Rescue ID E5P
Rescue Sequence 2
ATCCAGCCAAGATATCCTATCGTGCAGCTGAAACCCGAAACCCGAATCCGAGT
TCGAAACGAAACGAATCGCAGTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCT
CTCTCTCGCGTGTGTGTATGTGTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAA
TCTTTTTAGCTGAAAGAAAGCGCAACTTCAATTAGCGAAAAGCAAGAGTAGCT
AACAAAAAGAAAAGCGGATCGAAAAGTAAAGAAAAACAAAAAAAAAAAACA
AAAGCAACAAATCGAAATGGCAAGCGAAGTGGCCCAAATACCCGCCGAGGG
AAACGCCCGCAGTGGCGGCGGCGGAAAAATCAGAGGAGCCGGAAAAGTCAG
CGGCCCCGCCAGCGGACTCAGCGGCCGCTCCAGCTGCCGCCCCCGCAGTGGA
GAAGGCTGAGGATGCCGATGGCGAAAAAAAGGACGGCGAGGCCGGAAAGCA
GGACAAGCAGCAGGATGGC

Genomic hit, Accession No. CSC:AC020154

Associated ORF
Genscan ORF: ORF2 predicted sequences
>21:06:03|GENSCAN_predicted_peptide_5|415_aa
MASEVAQIPAEETPAVAAAEKSEEPEKSAAPPADSAAAPAAAPAVEKAEDADGE
KKDGEAGKQDKQQDGEEPKKDEAVAAPVATKSEAPPAQKFNVHKTNFEKDIIYL
YQFSRTPLLPSLSPYCLKVETWLRLVGLKYENVDHKMRFRSKKGQLPFIELNGEEI
ADSAIIIKELSSKYEKYLDSGLTAEQRNVSYATIAMLENHLIWIIFYWRAKYPDNV
LKGYKVNLQHALGLRLPNSILNFFFKITFGRKGTKKLKAHGIGVHSAEEIEEFGKD
DLKVLSEMLDCKPFFFGDEPTTLDVVAFAVLSQLHYLSKDIAYPLRDYMTEKCPN
LIGHVSRMKDKCFPDWDEICTKLDLNAHIPKPEPETKEGKEGGEQEKSNEQEGTE

GDKIEKELEKDKSNEKESTEENKEKEETK

>21:06:03|GENSCAN_predicted_CDS_5|1248_bp
atggcaagcgaagtggcccaaatacccgccgaggaaacgcccgcagtggcggcggcggaaaaatcagaggagccggaaaa
gtcagcggccccgccagcggactcagcggccgctccagctgccgcccccgcagtggagaaggctgaggatgccgatggcga
gaagaaggacggcgaggccggaaagcaggacaagcagcaggatggcgaggagcccaaaaaggacgaggcggtggcagc
acccgtggcgaccaaatcggaagccccgcccgcccagaaattcaatgtgcacaagaccaacttcgagaaggacatcatctatct
gtaccagttctcgcgcaccccactgctgccctccctgtcgccctactgcctgaaggtggagacctggctgcgtcttgtgggcctga
aatacgagaatgtcgatcataagatgcgtttccgctccaagaagggtcagctgccgttcatcgagctgaatggggaggaaatcgc
cgattcggccatcatcatcaaggaactgtcgtccaaatacgagaagtacctggactcgggactcaccgccgagcaaaggaatgt
ctcgtacgccacgattgccatgctggagaaccatctcatctggatcatcttctactggcgcgccaagtatccggacaatgtgctcaa
gggctacaaggtcaacttgcagcacgccctcggcctgcggctgcccaactcgattctgaacttcttctttaagatcacctttggtcgc
aagggcacgaagaagctgaaggcgcacggcatcggtgtccacagcgccgaggagatcgaggagttcggcaaggacgacctg
aaggtgctcagcgagatgctcgactgcaagcctttcttcttcggcgacgagcccaccaccctggatgtggtggccttcgctgtcct
ctcgcagctccactatctgtccaaggacattgcgtatccgctgcgcgactacatgaccgagaagtgccccaacttgattggccacg
tatctcgcatgaaggacaagtgcttccccgactgggacgagatctgcacgaagctggacctcaatgcgcacattcccaagccag
agcccgagaccaaggagggcaaggagggtggcgagcaggagaaatcaaacgaacaggagggcactgagggcgacaagat
cgagaaggagttggagaaggacaagtcaaacgagaaggagtcgaccgaggagaacaaagagaaggaggaaacaaagtaa

***Drosophila* Gene Hit**	rescue sequence and TBLASTN with ORF2: failed axon connections (U21685)
Human Homologue	BLASTX with fax: Metaxin 1 and 2 (Q13505 and AF053551)
***Drosophila* EST**	several including LD31362 (AA951078 similar by BLASTN to U21685 failed axon connections)

Annotated *Drosophila* genome genomic segment AE003527

Annotated *Drosophila* genome Complete gene candidate CG4609 – fax failed axon connectionsconnections

Human homologue of Complete gene candidate 4505281 ref|NP_002446.1|pMTX| metaxin>gi|3024205|sp|Q13505|MTXN_HUMAN METAXIN (4e-06)

Putative function Drosophila fax is a dominant genetic enhancer of the Abl mutant, developmentally expressed in axons of the CNS

Confirmation by RNAi Weak reduction of G1 and G2/M peaks indicating fewer cycling cells

Line ID	262/20
Category	Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle)
Reversion	NR
Map Position	72F

Rescue ID G6E

Rescue Sequence

AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG
GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA
ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTAGCGTTGCAGGCAGT
GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA
GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT
AGATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCT
AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT
TTTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG
ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAAAATTAAGAACA
TCTCCATTTATGTTCCC

***Drosophila* EST** several including LD28084 (AA949260)

All other results as for line 1466/4

Line ID 262/22
Category Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle)
Reversion NR
Map Position 72F

Rescue ID F1E
Rescue Sequence 1
AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG
GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA
ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCNAGCTAGCGTTGCAGGCAGT
GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA
GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT
AGATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCT
AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT
TTTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG
ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAAAATTAAGAACA
TCTCCATTTATG

Rescue ID F1P
Rescue Sequence 2
GTGCAGCTGAAACCCGAAACCCGAATCCGAGTTCGAAACGAAACGAATCGCA
GTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCTCTCTCTCGCGTGTGTGTATGT
GTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAATCTTTTTAGCTGAAAGAAAG
CGCAACTTCAATTAGCGAAAAGCAAGAGTAGCTAACAAAAAGAAAAGCGGAT
CGAAAAGTAGAGAAAAACGAAAAAAAAAAACCAAAGCAACAAATCGAAATG
GCAAGCGAAGTGGCCCAAATACCCGCCGATGAAACGCCCGCAGTGGCGGCGG
CGGGAAAAATCAGAAGAGCCGGAAAATCAGCGGGCCCGCCAGCGGGACTCTG
CGGGCGCTCCAGCTGCCGCCCCCGCAGTGGAGAAGGCTGAGGATGCCGATGG
CGAA

***Drosophila* EST** several including LD28084 (AA949260), LD38479 (AI518768)

Other results as for line 1466/4

Line ID	262/3
Category	Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle)
Reversion	NR
Map Position	72F

Rescue ID	H3E

Rescue Sequence

AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG
GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA
ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTATCGTTGCAGGCAGTG
TGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCAG
ATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAATA
GATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCTA
AATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTTT
TTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCGA
TCCTTAGGTTAAGTTTCGAGTTTCGCGACTAGATTTATTAAAATTAAGAACATC
TCCCTTTATGTTC

Other results as for line 1466/4

Example 24 (Category 3)

Line ID	238/20
Category	Mitotic defects in brain: metaphase arrest (overcondensation, metaphase with bipolar spindle
Reversion	NR
Map Position	75E1-3

Rescue ID D7E

Rescue Sequence

TTCAGTCGCGCATTTCACCGTTTCCGAATCGGACGAACCGGGCGTGATTGCTC
TCCTGCTGCTTTCGAGATCGGAGTCCCGATAAGGATATAACTACAACCTAAAG
AGGAATCCAAGCCTCCTCCTGCCGCTAGTTTCGAAAAGTAAATAGAGTACTTG
TTATCAACTGGGGAAGCGGAGATACATAGCTCCGATATTCCTGTGAAAGCCAG
ACAAACGGATACCAACGAACAATCGCCATGTGCGTCGTCGTCCCTTCTCGTTT
CACACATCGTGCGATAAAAATACCGCTTTGCTTTTTGTGTTTATTTAAAAATTT
TGGTTAGGAAGTGAACTCGAACTCGTGACGTTTGCATTTTCACAACAACAAAA
AGAGCAAAACATAGCAGAAGAACCCCAGAAGAAACAGGAACAGAAACCGTT
GACCGAGTGCCAGTGTGAAGGTCTAGGCACAAAGAACGCTACCAAGAACTCT
TGGGAGTTAGGGAGGCTCTTTACAATGACAACATTGCACCAAAGATGGACTCT
CTCTCTAAAATGCATTTCATACCAATATTTACTTT

Drosophila **EST** several including LP04802 (AI260815)

Annotated *Drosophila* genome genomic segment	AE003519
Annotated *Drosophila* genome Complete gene candidate	CG3979 - novel gene with homology to sodium-dependent dicarboxylate transporters
Human homologue of Complete gene candidate	3e-87 4506979 ref|NP_003975.1|pSLC13A2| UNKNOWN >gi|2499523|sp|Q13183|NDC1 _HUMAN RENAL SODIUM/DICARBOXY

Putative function sodium/dicarboxylate transporter

Confirmation by RNAi Only WT profiles observed

Line ID	490/9
Category	Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29)
Reversion	NR
Map Position	95C1-8

Rescue ID I4E

Rescue Sequence

GCTCTGCCGCTTCAACCGCCCGCGTTCTGTGTGTTGGTGTGCCGCGACGTAGG
TGTAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGCGAGAGCGGGAGAAGA
GCAGAACGTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT
AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA
TTATTGAAATCATTTATTTGATGGTCTATGGGGGTTTCTTTCGTAGTTATTCAT
AGATCGGCGATTTAAGCTACGCTTAAAGGGTAATTTGTCTGAGATATCTTTGT
CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG
CCAGCTTTTCAGCAGAGTTCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA
ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA
CCATTTGTACGTTTTAAATTAAAGTATTTTGATTTTCACTAATACAGGCTCTAA
GCTGATCCAAATCTACAAGCTTAGTTTTTGAATAGTCTTCACATGTTGACTTTT
ATTCTCT

Genomic hit, Accession No. CSC:AC015160

Other results same as 238/20

Line ID 660/3
Category Meiotic defects in testis: cytokinesis defects,abnormal spindles. (Ab-01/03)
Reversion R?
Map Position 75E

Rescue ID H8E
Rescue Sequence
GCTCTGCCGCTTCAACCGCCCGCGTTCTGTGTGTTGGTGTGCCGCGACGTAGG
TGTAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGCGAGAGCGGGAGAAGA
GCAGAACGTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT
AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA
TTATTGAAATCATTTATTTGATGGTCTATGGGGGTTTCTTTCGTAGTTATTCAT
AGATCGGCGATTTAAGCTACGCTTAAAGGGTAATTTGTCTGAAATATCTTTGT
CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG
CCAGCTTTTCAGCAGAGTTCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA
ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA
CCATTTGTTCGTTTTAAATTAAAGTATTTGAATTTC

Genomic hit, Accession No. CSC:AC015160

Other results same as 238/20

Example 25 (Category 3)

Line ID	273/18
Category	Mitotic defects in brain: metaphase arrest (overcondensation, very high mitotic index, few polyploids, metaphase with bipolar spindle)
Reversion	NR
Map Position	75E
Rescue ID	D1E

Rescue Sequence

AACTGGGCTAAAACCAGCTGAAAACTGGTGAAAAGTAAAATATTTGGAGAAG
GAAAGCCTTAAGTTCCTCTCTACGCTTCGTACACGTAATGTGCGTGGTTTAATC
TACGTTAAAACAAGTGGAAACCATGTTACGTGCCGTGGCTTTGTGTGTGTCAG
TGGTGCTCATAGCACTATATACGCCAACTTCTGGGGAATCCAGTCAGAGCTAT
CCCATTACCACGCTAATCAACGCGAAATGGACGCAGACGCCCCTATATCTGGA
AATCGCCGAGTATCTGGCCGATGAGCAGGCGGGCCTCTTCTGGGATTACGTTT
CGGGGGTGACAAAGTTGGACACGGTTCTCAACGAATATGGTTTGTGTTTATAA
GTCATGGAGAACCCGCATTAAAGAGCTTTTTATATTCTCCTCAATGTGAATCC
GAATCCATATAAAATC

Genomic hit, Accession No. AC015160

Associated ORF

Genscan: >ORF2 predicted sequences
>16:57:34|GENSCAN_predicted_peptide_5|1548_aa
MLRAVALCVSVVLIALYTPTSGESSQSYPITTLINAKWTQTPLYLEIAEYLADEQA
GLFWDYVSGVTKLDTVLNEYDTESQQYNAALELVKSHVSSPQLPLLRLVVSMHS
LTPRIQTHFQLAEELRSSGSCQSFTFAQVGSELACSFNELQKKLEVPLAKDSLDAS
VVTYSFDHIFPGSENNTRTVVLYGDLGSSQFRTYHKLLEKEANAGRIRYILRHQLA
KKDKRPVRLSGYGVELHLKSTEYKSQDDAPKPEAGSTSDEDLANESDVQGFDFK
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LQILQYTAHNFPMLARTLLAHKVTDGLRAEVKHNTEAFGRSLNVAPPDGALFING
LFFDADTMDLYSLIETLRSEMRVLESLHSNNVRGSLASSLLALDLTASSKKEFAIDI
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QPTARSVIKLSESFVIHQAPIRLGLVFDARDANEDNLADYVAITCAYNYVSQKKD
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THALDYVQSGESVRVAFIPNTESSSASSRRNLNRLVWAAMQSLPPTQATEQVLK
WLKKPKEKIEIPTQLEDILGSTELHLKMLRVYSQRVLGLNKSQRLVIGNGRLYGPL
SSDESFDSADFALLARFSSLQYSDKVRQVLKESAQDVNEEFNSDTLLKLYASLLPR
QTKTRFKLPTDLKTDHSVVKLPPKQENLPHFDVAAVLDPASRAAQKLTPILILLRQ
VLNCQLNLYLIPVPQHSDMPVKNFYRYVVEPEVQFEANGGRSDGPLAKFSGLPAN
PLLTQQLQVPENWLVEAVRAVYDLDNIKLTDIGGPVHSEFDLEYLLLEGHCFDAA
SGAPPRGLQLVLGTQSQPTLVDTIVMANLGYFQLKANPGAWSLRLREGKSADIYA

ISHIEGTNTHHSAGSSEVQVLITSLRSHVVKLRVSKKPGMQQAELLSDDNEQAAQS
GMWNSIASSFGGGSANQAATDEDTETINIFSVASGHLYERLLRIMMVSLLKHTKSP
VKFWFLKNYLSPQFTDFLPHMASEYNFQYELVQYKWPRWLHQQTEKQRTIWGY
KILFLDVLFPLNVRKIIFVDADAIVRTDIKELYDMDLGGAPYAYTPFCDSRKEMEG
FRFWKQGYWRSHLMGRRYHISALYVVDLKRFRKIAAGDRLRGQYQALSQDPNS
LSNLDQDLPNNMIHQVAIKSLPDDWLWCQTWCSDSNFKTAKVIDLCNNPQTKEA
KLTAAQRIVPEWKDYDAELKTLMSRIEDHENSHSRDSAVDDSVDDSVEVTTVTPS
HEPKHGEL

>16:57:34|GENSCAN_predicted_CDS_5|4647_bpatgttacgtgccgtggctttgtgtgtgtctgtggtgctca
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taaactgtcagagtcgtttgtcatccatcaagctcccattcgcttgggtttggttttcgatgcgagggacgccaacgaggataatcttg
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gatcatgagaattcgcatagcagggactcggcagttgatgattcggttgacgattcggtggaggtcaccactgtgacgccttctcat
gagcccaagcacggcgagctgtga

***Drosophila* Gene Hit**	rescue sequence and BLASTX with EST and TBLASTN with ORF2: UDP-glucose:glycoprotein glucosyltransferase (U20554)
Human Homologue	BLASTX with UDP-GGT: hypothetical protein (AL133051)
***Drosophila* EST**	several including GH16576 (AI293351)

Annotated *Drosophila* genome genomic segment	AE003519
Annotated *Drosophila* genome Complete gene candidate	ugtUDP-glucose-glycoprotein glucosyltransferase

Human homologue of Complete gene candidate	CG6850- IGI_M1_ctg14521_41 D65BCE6EEC187AE3 TRANS:SEPT20T.ctg14521.2 2 FPC_ctg:ctg14521 FPC_start:1284609 FPC_end:1284696 FPC_strand:+ (1.20E-215)

Putative function ugtUDP-glucose-glycoprotein glucosyltransferase

Confirmation by RNAi Only wild type profiles observed

Example 26 (Category 3)

Line ID	430/5
Category	Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle)
Reversion	NR
Map Position	98B5-8

Rescue ID 2C2E

Rescue Sequence

GTGCGGCCCATGGATGTGCGAACGTGTACGAAGACCAAGATCGGCATCGCCA
TCGGCGGCAGCACGACGGACGATAACGAAAAAGCTACAGCCGCCGCCACAGA
TACAGATGCAGATGCCATGCCGCTGTTATCAGCGCGAGCGGGAGAATGATAA
GGGATGGGATCGCTCAGCGCGGCAGGCAAGACGACCAAAAAGAGAGCCAAC
TAAATGATGTGCCTAAGACTAAGAGTTTAATGAGCATTACTGTCGCGCACTCT
ATGTATTATGAATAAAATTCATACAACTTTTGTGGTTTATTATAATATAAAAGT
GTGTCAGCTCTACTCGGGGGAAAGTAAGTTTACTTCTTGGCCGCTGGCTTCTTG
GCGGCGACCTTCTTCTTGCGGGCGGCCAGCAACTTGGCGCGATTGGCGCAGCC
TTGGTGGCCACATTGGCGAAGTGCGACTTGGCCAGCTCGACGTTCTGCTTCTT
GGCTTGGCCAGCACCTTGGCCACGGTGCGCTTCTCGGCGGCGAGGGCGGCAC
GACGCTTGAGTACCTCGGCATAAGGGTTCAACTTGATCAACTTGCGCACGGTT
GGTAAGGGGGTT

***Drosophila* EST** several including LD45359 (AI513164)

Annotated *Drosophila* genome genomic segment	AE003763
Annotated *Drosophila* genome Complete gene candidate	CG5502 RpL1 - Ribosomal protein L1
Human homologue of Complete gene candidate	1e-126 432359 dbj|BAA04887| (D23660) ribosomal protein [Homo sapiens]

Putative function structural protein of ribosome involved in protein biosynthesis

Confirmation by RNAi Marked decrease in G1 and G2/M indicating fewer cycling cells

Example 27 (Category 3)

Line ID	472/12
Category	Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles (mitotic: High mitotic index, meiotic: Ab-08/24)
Reversion	R?
Map Position	96C7-9

Rescue ID 2B6E

Rescue Sequence 1

GTCTGACGTTCTCTGAGGGCAAAAGTTTCGAGTTAGTTGAAGGTGAGGGTGCT
CGATCACCGATTTGCGGTGAGACGAAAGAAAAGTATGCATTGTTGCGTTGTAA
AGAGAGCCGGCGCTCGTCTTGTTCACATTGTCGCTGAGAACGTATGTTGTGCT
TCATCATTTCCTTGTTGATTTCCCTTTGACGTGGCAACTTGACCATGTATGACA
ACTCTTTGGTGGTGCCATCTGGAAGGCAGAAATTTGATGTCAACGGTGCTCCC
AGCCAGTCCACTCCCCAACTCACCCTGCAGCTCCACTTCGATATTAACTCGCA
ACATATTAGTGGCGTAGTTGTCACCTGCCGCGGATCCCATTTCCGCTTTGAAAT
TTCGCACTTTCGAATATCCGTCCACATTCGATTTGAGAACATCTTCGAAACGTT
CAGCGGTGACCCAATCGGGTATTTTGCCAGCCGCCATTGTAGATAATCGGGAT
AAGTATTTTGAAATCGAGCAGAAAACACATATACGTCCAGTGTGACGGTCTTG
CGTAGACTGATGAAAGCCGAGTATTAGACTCTACACATCTGTGGAGCTTTTTA
ATTTCGTAGTGCGCGGCCGATTTCTCTCGATCTTCTCTCAAAAGCTCCGCTAAT

Annotated *Drosophila* genome genomic segment	AE003751
Annotated *Drosophila* genome Complete gene candidate	CG10618 - novel
Human homologue of Complete gene candidate	none

Putative function no homologies which indicate function

Confirmation by RNAi Only wild type profiles observed

Example 28 (Category 3)

Line ID 571/15
Category Mitotic defects in brain: metaphase arrest (overcondensation, few anaphases, some polyploids)
Reversion NR
Map Position 93D

Rescue ID 2A8E
Rescue Sequence
GGCGGCGCTACATTTGTTGTTGTCGCTGCTGCTCACAGCTCCACCACCATTTGC
ACAGTTATATTACCTCGCTCAAGTCGCCCCTCTCCCTCTCGCCCACTCGCTGTG
TCAATCGAATTAAAACGAATGCTCTTCGGCGAATAATTGGGTTTAGATACTTT
TCCAGCAGACAAAGTTGTATTTTTTGCACTTCTTATTGATATTAGGCAAAACGC
ATCGGCCGAATCACACGCACACAAAGCACACACGCGAGCAGCGGTTTTTCAA
TCTGCAGTACACCAAACAACACACACTATTTCCTAATGCCTGTTCTTATCCCTC
TGATATTCCCAATGAATCGCTGGGCAATTGGCGATTCGAACCGATTTTCACTT
GGCTCTTTGTTTTATTTAATTTTCACCGAAACGCTCTCACACGCAGAGACGCTT
TTGCTCGTTCGCTGATGCTTCTGCTGCAATACACACCACCTACGAAACGAGCC
AAGGGAAATTGTATCTATGGGCTGTGTATCTGTTTCTACGCGGCACGCGCTGC
ACGTCCGCTCGCTTCGGGTTTTCGAGAGAGAATATAACTTTTTCGATACGGTA
CGGTAAACGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATA
CGCCTATTTTATAGGGTAATGCATGATAATAATGGGTTCTTAGACGTCA

***Drosophila* EST** LP07504 (AI294185), LP06548 (AI293427)

Annotated *Drosophila* genome genomic segment AE003734
Annotated *Drosophila* genome Complete gene candidate CG15802 – novel homology to Doom, a product of the Drosophila mod(mdg4) gene, induces apoptosis and binds to baculovirus inhibitor-of-apoptosis proteins

Human homologue of Complete gene candidate none

Putative function inducer of apoptosis

Confirmation by RNAi Only wild type profiles observed

Example 29 (Category 3)

Line ID 736/15
Category Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar spindle)
Reversion NR
Map Position 73C

Rescue ID H5E
Rescue Sequence
CTAATGAGTAAGGAAAACCAATCAGCCTTGCTAATCGCTTGGCAGTATTGGCT
TCTATGCAGGGGGGCGTGTCCCGCGCCCCTTGAAGCTCAAATTTTTGCAAGGG
CACAGGTCGTCCCCTCCTCCTCCGCGTGGGTGGCGTTCGGCCGAACGAACCGG
CGCCTACTTTGCGTCCGGCTAGCGAGGATCTCTGGGTGCCACCCCACGGCTGG
GTGTTGCGATCTGCCCGATTGATAATCCATGCGTGAGAAAGCTTTAGAGAATC
TGCCAGATTATTATTACTCCCCGCATACTCAGAAAAATGTATCCTTCAGATATG
TTTATGTTTATGAAGTGAAAAAAGTCCTTTGAAATACTACAAAAAGTGAGGAT
CTGACCAATGATTTGATTTCTATAGAAATATACTATAAACTATAAACTAC

Genomic hit, Accession No. CSC:AC014181

Annotated *Drosophila* genome genomic segment AE003526
Annotated *Drosophila* genome Complete gene candidate CG3971 baldspot - with homology to membrane glycoprotein

Human homologue of Complete gene candidate CG3791-9e-08 4680391emb|CAB41293.1| (AL034374) dJ483K16.1 (novel protein) [Homo sapiens]

Putative function membrane protein, function unknown

Confirmation by RNAi Slight reduction of G1 and G2/M peaks indicating fewer cycling cells

Example 30 (Category 3)

Line ID 82/24
Category Mitotic defects in brain: metaphase arrest (condensation, no polyploidy, no anaphases, metaphase with bipolar spindle)
Reversion NR
Map Position 100D

Rescue ID 2E3E
Rescue Sequence
GGTCAAGCCCGATGGCGTCCAGCGCGGGCTCGTCGGCAAGATCATCGAGCGC
TTCGAGCAGAAGGGCTTCAAGCTGGTCGCCCTGAAGTTCACCTGGGTAAGCGG
ATAATTGAATTAGGAAGAAATCAATAGATATACATACGTGGAAACGGGTTGC
CCCACGCGGGGTTGCTATCGGACCTAACCTCAAAGGCTGGGTGCAGGCGTCAT
CGCGGAATGACATGTGTTTAGAGGTCAGAACTGCAATTAACTGATAACGAACC
GTTTTGTAACCAGGCCTCCAAGGAGCTGCTGGAGAAGCACTACGCTGATCTGT
CCGCCCGCCCCTTCTTCCCCGGACTCGTGAACTACATGAACTCCGGCCCCGTG
GTGCCCATGGTGTGGGAGGGTCTGAATGTGGTCAAGACCGGTCGCCAGATGCT
CGGCGCCACCAACCCCGCCGACTCGCTGCCCGGCACCATCCGCGGTGACTTCT
GCATTCAGGTCGGACGCAACATCATCCACGGCTCCGATGCCGTCGAGTCTGCC
GAGAAGGAGATCGCCTGTGGTTCAACGAAAAGGAGCTGGTCACCTGGACCCC
GG

Genomic hit, Accession No. CSC:AC012727

Associated ORF
Genscan ORF1 predicted sequences >16:43:49|GENSCAN_predicted_peptide_7|172_aa
MKLLMLGTILAFFSVISATMAANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLV
ALKFTWASKELLEKHYADLSARPFFPGLVNYMNSGPVVPMVWEGLNVVKTGRQ
MLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAEKEIALWFNEKELVTWTPA
AKDWIYE

>16:43:49|GENSCAN_predicted_CDS_7|519_bp
atgaagctcctgatgctcggcacaattttggcattcttttctgtaatctcggcgacaatggcggctaacaaggagaggactttcatcat
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tgaagttcacctgggcctccaaggagctgctggagaagcactacgctgatctgtccgcccgccccttcttccccggactcgtgaa
ctacatgaactccggccccgtggtgcccatggtgtgggagggtctgaatgtggtcaagaccggtcgccagatgctcggcgccac
caaccccgccgactcgctgcccggcaccatccgcggtgacttctgcattcaggtcggacgcaacatcatccacggctccgatgc
cgtcgagtctgccgagaaggagatcgccctgtggttcaacgaaaaggagctggtcacctggaccccggccgccaaggactgg
atctacgaatag

***Drosophila* Gene Hit** rescue sequence and TBLA: abnormal wing disc (awd) (X13107)
Human Homologue BLASTX with awd and TBLASTN with ORF1: tumor metastasis inhibitor nm23-H2 (A49798) non-metastatic cells 2, protein (NM23B) (P22392) and nucleoside diphosphate kinase B.

***Drosophila* EST**	several including LP05977 (AI257573 similar by TBLASTX to X92956 B.taurus mRNA for nucleoside diphosphate kinase (NBR-A)

Annotated *Drosophila* genome genomic segment	AE003779
Annotated *Drosophila* genome Complete gene candidate	CG2210 - awd abnormal wing discs nucleoside diphosphate kinase
Human homologue of Complete gene candidate	gi4505409 1A5C3F84D7AD272C |ref|NP_002503.1| non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens] (1.90E-61)

Putative function human nucleoside diphosphate kinase, transcriptional regulation of c-myc expression.a candidate suppressor of tumor metastasis

Confirmation by RNAi Only wild type profiles observed

CATEGORY 4: ANAPHASE DEFECT

Example 31 (Category 4)

Line ID	1132/8
Category	Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes)
Reversion	?
Map Position	86F3-6

Rescue ID 2C3E

Rescue Sequence

GGCCGGAGGTACCATTTTGGTAGGACCGTTTTTCGGGCCAACGAAAATACCAC
AAGACGGCAGCGATAATAGTGTTTTTTGCTTCAAATGTAGTATGGCTACGCAA
CTCACATATGGTTAAGAACTTCGCTGTTTATTTGGTGGTTAAACTAGCTAAATA
CAATAAGAGTGGCAACGCCGTCACGTTTTCTACATGTATTTTACTTGGCGTAGT
GCGCCAAGCTTATAAACCACAGTTGGGCGGTTCTTTTGAATTGTTTAATTTACA
CCCCACTATGAAACTTATTAGCCTTCTTTATTTATTTTATATTTTATTTTTAGGA
AGAATACGTTTACTCAAGGTTCGCAGCTTGTCAATCAGTATTCGCAAATATCA
ATAATAAAAGGCATCAATTTTCCAATCAGCAGTTGAAAAGAACTCCCCTCGAC
ATTTGAACAAAATGCATTTTTGGGTGATTATAATTTATTAGAATTTTTATTGAC
TTAAGGTAAATATAAATAAAATATTATTCAAGTACAAAGGTATATATACTCAT
TAATANTATTTGGATTCAAGGAAAATATATTTCAAAATGGCGGGGGTTTAATA
AAACAATTTTTCAAATTAAGG

Genomic hit, Accession No. AC007805

***Drosophila* EST** several ESTs including LP09688 (AI295922)

Annotated *Drosophila* genome genomic segment AE003693
Annotated *Drosophila* genome Complete gene candidate CG6929 - Lk6 kinase

Human homologue of Complete gene candidate gi4505191 DB39E49EC0BED990 |ref|NP_003675.1| MAP kinase interacting kinase 1 [Homo sapiens] (6.20E-113) and gi9994197 551A82FA3D09FD58 |ref|NP_060042.1| G protein-coupled receptor kinase 7 [Homo sapiens] (1.70E-106)

Putative function Protein kinase associated with microtubules

Confirmation by RNAi Complete loss of G1 and G2/M indicating fewer cycling cells

Line ID 483/19
Category Meiotic defects in testis: segregation defects
Reversion ?
Map Position 86F

Rescue ID H2S
Rescue Sequence 1
CTCCGGCCACACGGATGAATTCGTCGTCATTCGTCGGAATCATTCGAACTTTG
AAAATGGATCGGTAGCTGGGAAGGAAACTTAAAGCGAAATACGCAAAGAAA
ACGGCTTTTGTCCGCTATTCAGCGATTTTTTTTGTGTTGTAATCAGCAGAGGAA
ATTTTAACGACCAACTCCACCGCCACACCAGCCATCTCCAGCAGCCCCGGAAA
ATAAAATAGAACTAAATTAACGCCACCATCACTACAACAACCATCTCACCAAC
AACTACAAGAGCAACAACCACAGCAACAGCACTACTGCACCAAGCCCACAAA
GAAGAGGTGAAACGCAATAATCGA=CAATACCCGAAGAAAAAAACAAAAAA
ATATCGCAGATAACCGAAAAAAGCGGTGCAATAGATAAACCCCATTTTTTGCT
TGAGCTTTTTTCGCCTGTGTGATGAGAGAAATCAGCAGCAGCCATCGATTACA
ACAACAACAGCAGCCACACCAACGACGACTCACCACCAAACGAAGAATAATA
ACCAGCGGANAGCGATAGATA

Genomic hit, Accession No. CSC:AC018284
***Drosophila* EST** several including GH28825 (AI517767), LP04213

Other results same as 1132/8

Example 32 (Category 4)

Line ID	1422/14
Category	Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect
Reversion	NR
Map Position	90B4-8

Rescue ID 2F1E

Rescue Sequence

GGCCAGCTGCTCAAACATTCTGCAGCTATTTGGCCGCCAGCGAGTAGAACGAT
ATTGCCAAATATTTTATAATAGTAACCAATACGTTACCAGTATGACCGCGCCG
ATAACGATAGAAAATACCACACGGTCTAAAAGTAAATACCATTTGGGGTATTC
CCTAATCTTTTGAATTATTTACCGTTAGGTTTCGGTCGTTTTTTTTTGTCAGCTG
TTCTTTGTATGAAACGGATTAGTAATTTTATTTGTTGTTTTTGTGCATTTTTGCA
TATTAAAAGCCTTGAAACATGCCTTAAATCGTTAAAATAGATTATAAGAGGGA
TGGACTGTTTGTTAAAACCAATTGGAAAATTTGTAATCGCTGGTAATAACTAT
CGAGATAAGCTTAATTATCGCTGTTTTCTTTGTATCTAGTTATAAATAATAATA
ATAAAACTGGTAATTAACAAAAGTAAAAAGTTACTTAACTTATACAAAAATAT
TTAGTTATTGNATTCAATAATAAGATGGTAATAATAGATGGTAAGATAGTAAT
ATTTTAATAATTGAATTTCATCACACATGCTGGTGCACGTTCCACAACTTACAA
TCAAACGAAA

Annotated *Drosophila* genome genomic segment	AE003718
Annotated *Drosophila* genome Complete gene candidate	CG7623 - novel with homology to UDP-galactose transporter.

Human homologue of Complete gene candidate	2136348 UDP-galactose transporter related isozyme 3 - human >gi|1669564|dbj|BAA13527| (1e-36)

Putative function sugar modification protein

Confirmation by RNAi **Slightly reduced G2/M**

Example 33 (Category 4)

Line ID 1479/10
Category Mitotic defects in brain: anaphase defects (overcondensation, anaphase bridge, metaphase with swollen chromosomes and bipolar spindle)
Reversion NR
Map Position 69F3-7

Rescue ID 2D6E
Rescue Sequence 1
CCACGGGCAAATGTGGTCCGGAGGTCCACGACAACGTGCCGCTGACCATATC
CCAGATTGAGCGCGCAACTCAGGATCCGGAGAACGAGAATGTGTTCATCACA
GACGACGTGCATCCGATTCACTTCTGCACCTGCATCATCTACGCCTTTGTAACT
GGCAATGGAACGCACAACGAGTCGTTCATGAAGTTCATGATCGATGATGGCA
CCGGCTCCCTGGAGGCCAGCATCACCAAAAAACCCTTCAATGGACGCGTGATC
AGCAGCCTGTACAGTGAAGCCAGTTCGCTGGCCTCGTCCGAGGCCTACAAGA
GCATTGCCGTGAGCATGATGCGGCTGCTGCAGGTCTCCATGGAGTACATTGAT
CCCACGCGCATCTCGAGGGGCCACAGCCTATTCCTGCGCGGTCGTCCGAATAG
GTTCCGCGGCAAGATGGGTCTGGACGCTTTTCAGTTCTTCATAGACAGCGGCC
GATCGCGGAATATGGAAATTGGCTTCGTGGACTACCTAACCGACTGGCAACG
AAGGCATAAAACAATGCAAAATAC

Rescue ID 2D6P
Rescue Sequence 2
GCCCGTGGACTTTTCACTCTGTTGATTCTTGCGTATCACGAAGTTATCCAGCTG
GCTTTCTATGTCCTCGAAACTCTGATTAAAATCCATTCTATTTGCTTAGTCTGC
GATTTCAAAGGGGATTTCTTTATTGCAGTGCATTTTGCATTAGCGCCAAAAAA
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ATTAAAATTAATTTTGTGAGCAATTTTCACACAATTGTATTATAAGTTAAAACC
AGGGTCACATTAATTTGCAGAACCGCGCAATATTTTCTTTTAACCCCCTTACA
AATTTTCAGTTGTTTTGACTACGCCCCTGCTAATTTTTACTTATTAAATTCAAA
GTCTAAAAACATTGTCACCAGATAATACGAGTATACACTATATGGACAAACGT
AAAATCGTTAATAGAATATATATATTCAACCATTATTTCACCACCGAGAGAAA
TTCATTTGCACAAAACGCCAGGTTGGCAGCACCATCATTGCGCACAGCAAGTG
GGCAAACTCGTTGTATCGCTTG

Genomic hit, Accession No. AC007328

Associated ORF
Genscan ORF1 predicted sequences >17:42:01|GENSCAN_predicted_peptide_2|1507_aa
MKLAPTVKLNNGYEMPILGLGTYNLKKSRCEAAVCHALEMGYRHIDTAYLYRNE
GIIGKVLAKLIGDQKLKREQVFLVTKLWDIYHEPKMVKYACDMQLKLLGVDYID
LYLMHSPVGVDYISDEDLMPHENGQLRTNDVDYVDTYRSMEQLVHLGLVRSLG
LSNFNANQLKRLLENCQIKPANLQIECHPELVQVPLIELCKFHNITVVAYSPLGRSQ
TCNPLPDYYTDSKLLALAAKYGKTPAQIILRYLSKDNEGEAAVKHAIDVGYRHID
TAYFYQNEAEVGKAIRDKIAEGVVKREDIFLVTKLWNIFHDPERVEGICRKQLSNF
GLDYIDLYLMHMPVGYKYVDDNTLLPKNEDDVLQLSDVDYLDTYKAMEKLVKL

GLRIEQLAGLSHLSTHSDGMQFRIRMFLTFQRGGPSHNNMQQQQQRGGGSGTDF
YNQQRDRRDSGRQMDNNYSNNYNNNNNNQRNRGGGNGMQQQQRGGNGGSGG
GGGNGGGNNPAWNMHRGNQNSNNMMNMRNRGMGSRGPMRPNQVHLLVTHT
AIDGLLNPGFHILQGYRPQSANNQNKPRNKIKFEGDFDFEQANNKFEELRSQLAKL
KVAEDGAPKPATNATAATATATNEQVGEKVEGVHTLNGETDKKDDSGNETGAG
EHEPEEDDVAVCYDKTKSFFDNISCEAAQDRSKNKKNDWRQERKLNTETFGVSS
TRRGSVAHQLNVFQAVTADATNTTTIMATAALTRDMEERQATTGTIIAWVGGGG
NFRNRSNNRNNGGGRGGNGMPNITNGNTAAALKAANNAAGHGSNATDSSAPNA
TTATTKSTSLLPEQTQQVAAVSLPVLLPSIGWLFIVMDGPPDIPRSADIAILFVSFEQ
SVLFLKFHKRYNEFAHLLCAMMSFEDIESQLDNFVIRKNQQSEKSTGKCGPEVHD
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tgcgtgcactgcgagaaaaagggagggggccatggagtggatgtga

***Drosophila* Gene Hit** BLASTN with rescue sequence 2: Histone acetyltransferase GCN5 (AF029776) very small match at end, TBLASTN with ORF1: middle domain histone acetyltransferase GCN5 (AF029776). Genomic matches histone acetyltransferase

Annotated *Drosophila* genome genomic segment	AE003541
Annotated *Drosophila* genome Complete gene candidate	CG4107 -Pcaf /GCN5 histone acetyl transferase transcriptional activator protein
Human homologue of Complete gene candidate	gi6382076 72F516F8BD10CD0C |ref|NP_003875.2| p300/CBP-associated factor [Homo sapiens] (1.20E-197)

Putative function Transcriptional activator

Confirmation in RNAi Only wild type profiles observed

Example 34 (Category 4)

Line ID 184/5
Category Mitotic defects in brain: Anaphase defects. (overcondensation, aneuploidy, some lagging chromosomes and breaks)
Reversion R
Map Position 71B

Rescue ID C4E
Rescue Sequence
CTCGAGCAGATGTGGGACGAGCTGAGCGGAGCGCACAAACTGCCAAGTAAGT
GGAGCATGTGGATGAAAGGAGTTCCCAGAACAGTGTTGCCAACCAAAAAAAA
AAAAAAGTTAAAAAGTTAATTTTAATAGTGTAAATAAATATGAATTAAATTAA
ATTTTTATGTAAACAGTATTAGCTTTACATGAGATTACCAAATTGTGAGTGTCT
GTGTTTGTTTGTCTTTTAAAAACTTTAAAAGCACATAAAGAAATATATTTTAAA
TTTAATTAAAAAGTTCGTAAAAAGTAAAAGGTAGCTAAATTAAAAAGTTTCCT
ATTCAAATCAGATTTGGCGAACAAAGAGCCAAGTTGGCAACACTGACAATGA
CTCCAAGCGCGAACAAAGCGATTTCTATCGTTATCCCACTCTCTCTCCCAGAG
ATCGTTCTCAAGGCCAAATGGAAGGGACTTCGAGACAATTTCCGTGTGGAGTC
AAAAGGATCCGGCGGCCGAATAACGG

Genomic hit, Accession No. CSC:AC019852

Associated ORF
Genscan ORF1 predicted sequences >22:43:26|GENSCAN_predicted_peptide_2|1003_aa
MAPKKSTIVLNVEQFIHDIEERPAIWNRNFHCNKAFLEQMWDELSGAHKLPKIVL
KAKWKGLRDNFRVEYKRIPRADNGDFMVDPATFESKWLHYYALLFLTDHMRHR
LPKNEQDQSFYFSQQSEDCEKTVVEPDLTNGLIRRLQDSDEDYDEEEMEADGEAS
EATMEETMPTPPAAHQMNQVSTTPLATGALRAQEEAHQHALIKAGLLRAQLMEL
EKEAEDLSRKPPPPQQMTSPVAPSLQVLVEPPAAHCSPPPMVTTTSAQVQQPGSA
AVLAPATTTSASSVSSNGAPMGGKRSVSPPPLYNKAHHPLATLAAAHLAAKDRN
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ITDAIQEWVERVAQTPVQGSSKPQVCIVELGGTIGDIEGMPFVEAFRQFQFRVKRE
NFCLAHVSLVPLPKATGEPKTKPTQSSVRELRGCGLSPDLIVCRSEKPIGLEVKEKI
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WRDLARRTETVRREVCIAVVGKYTKFTDSYASVVKALQHAALAVNRKLELVFIE
SCLLEEETLHSEPSKYHKEWQKLCDSHGILVPGGFGSRGMEGKIRACQWARENQ
KPLLGICLGLQAAVIEFARNKLGLKDANTTEIDPNTANALVIDMPEHHTGQLGGT
MRLGKRITVFSDGPSVIRQLYGNPKSVQERHRHRYEVNPKYVHLLEEQGMRFVG
TDVDKTRMEIIELSGHPYFVATQYHPEYLSRPLKPSPPFLGLILASVDRLNQYIQRG
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>22:43:26|GENSCAN_predicted_CDS_2|3012_bp
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aaaattcccattacacccacaaatggaatatcaaaaagttgcaatggtagcataagcacttccgacagcgaaggtgcctgcggag
gcgttgatcctaccaatggccataagtaa

Human Homologue TBLASTN with ORF1: CTP synthase (CTPS) (NM_001905.1)
***Drosophila* EST** LD27370 (AA941993)

Annotated *Drosophila* genome genomic segment AE003532
Annotated *Drosophila* genome Complete gene candidate CG6854 - novel protein, possible CTP synthase?

Human homologue of Complete gene candidate gi4503133 C33BD849A0044697 |ref|NP_001896.1| CTP

	synthase; cytidine 5-prime triphosphate synthetase [Homo sapiens] (8.40E-217)
Putative function	Enzyme important in the biosynthesis of phospholipids and nucleic acids, and plays a key role in cell growth, development, and tumorigenesis. The region of the human gene is the location of breakpoints involved in several tumor types
Confirmation by RNAi	Loss of G1 and G2/M peaks indicating fewer cycling cells

Example 35 (Category 4)

Line ID 225/27
Category Meiotic defects in testis: segregation defects
Reversion NR
Map Position 90D

Rescue ID 2D2P
Rescue Sequence 1

Rescue ID 2D2E
Rescue Sequence 2
GCCTGAACTTAAAACGCTGCCTTCGGCTCTCGCTCGGCACTCGCTCGGCTGCG
ACGTCGACTGCGACGCTGGCAGCGACAACAACGATTGGCCTCTCTCATTCACT
TACCTCCTCTCTCTCTCTCGCACTCTCTCTTAGCGGTGAGAGAGTGTTTTCCTC
ACATTTGTTTTGCTTTTGCGGTTCGCCAATGGCCCCCCAAAACGAAAAGAGCG
CGCAAGAGCTAGCTCCACAGTGGATCCTAAGAGAACGGTCCCTGTGGACTCC
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GTGACCACTTCAAACATGAAAGCGAAATGTCCTGAGACCCTACAAAAACTAG
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TTTCGCCATAATTTACACTATCTAAGCTTTTATTTTTAGCCACATGATATATGC
ATGCA

Genomic hit, Accession No. AC008361

Associated ORF
Genscan ORF1 predicted sequences >20:36:39|GENSCAN_predicted_peptide_2|515_aa
MSSTIRLQTSSCQCCKLYKYERHPNKPNLQPTPIPNYPCEILHIDIFALEKRLYLSCI
DKFSKFAKLFHLQSKASVHLRETLVEALHYFTAPKVLVSDNERGLLCPTVLNYLR
SLDIDLYYAPTQKSEVNGQVERFHSTFLEIYRCLKDELPTFKPVELVHIAVDRYNT
SVHSVTNRKPADVFFDRSSRVNYQGLTDFRRQTLEDIKGLIEYKQIRGNMARNKN
RDEPKSYGPGDEVFVANKQIKTKEKARFRCEKVQEDNKKNRNGKAAGGKGKTR
RVARGAQIYQNWAICRNLFLFLSLACCRVCKVCDIVVEFRKGTNAVVNVQIREAI
SHVFHKEDIVIDVQESKEWCIWTDDQVQSPLPELENLWHELWIGPSHAYLIDQIVD
LFENLLEKYNVQVVDVVRFNFLHRALVVVIISGIIIIIIIMIIGVSGGQRTNAFSHHRS
QRSAIGGDPQQKDSAVQQVQARSSDAFCQIPHRSPRFPGRSQLIPKPNREILRNASA
TKNLLFRIRSQ

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***Drosophila* Gene Hit** BLASTN with rescue sequence: couch potato (Z14974).
Human Homologue BLASTX with couch potato: RBP-MS/type 2 (RNA binding motif family)(D84108)

Annotated *Drosophila* genome genomic segment	AE003720
Annotated *Drosophila* genome Complete gene candidate	CG18434 -couch potato RNA binding protein
Human homologue of Complete gene candidate	2224621 dbj|BAA20798| (AB002338) KIAA0340 [Homo sapiens] (2e-19) and Ensembl predicted peptide Gene:ENSG00000070877 Clone:AC009710 Contig:AC009710.00004 (predicted unknown protein)

Putative function Possible RNA binding protein

Example 36 (Category 4)

Line ID	238/37
Category	Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/17)
Reversion	?
Map Position	70D

Rescue ID	I7E

Rescue Sequence

GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC
TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG
TCTTCGCTCCATTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT
GATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG
CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG
GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG
ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG
TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGA
GAATGATCTGGTCAAGTGTGCGCTCATCGCTGACGTTCTCAACCTGCGCAGCG
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TTCGCCTGCTTGGCGGCGTGG

Genomic hit, Accession No. CSC:AC017664

Associated ORF

Genscan ORF1 predicted sequences >15:26:30|GENSCAN_predicted_peptide_1|1819_aa
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NNSEDKLKKIKSDLRHAQEAFKECVEYFGDSSRNADAAAFFALIVRFTRAFKQHD
QENEQRLRLEKAAALAASKKENDQVLMRNKVNQKKQQEAVINELKSKAHSVRE
KKLLQQDEVYNGALEDILLGLKSEPYRRADAVRRSQRRRIDNNRLSRTLEEMDCL
HENDLVKCALIADVLNLRSVHVTPVSSKDWEIIELSTEKISGSVLEQTRIVNSTQILI

VWINKSMQVALTVDRLKPHMNYGRIDHNTELVVAPNLYKGLTNGTSNGVIEENT
KLSRSKTTAQVKDELTEKLTPLTHSSTVSNVKNTIQRNKRQDHMERLKKDLRRES
SRSFEFRVIRGLWREQAQESDVFVNGKHLPEFFDLDLFYCMHTAADKDYYVRVR
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AQFLKESKIYAADLVRPVGEIIKEETPPTSPLSVQDLIQLPEYDKIVDQVVQELRMN
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agcttggcgccgaaacgtggtcacgattccacgggggtcaccgatcgagtg

***Drosophila* Gene Hit** recue sequence and TBLastn with ORF1: mRNA for l(3)70Da (AJ243811)

Human Homologue BLASTX with l(3)70Da: peroxisome biogenesis factor 1 (AF026086)

***Drosophila* EST** LD43687 (AI512050)

Annotated *Drosophila* genome genomic segment AE003536

Annotated *Drosophila* genome Complete gene candidate CG6760 mRNA for l(3)70Da - novel protein with homology to endoplasmic reticulum ATPases

Human homologue of Complete gene candidate 4505725

	ref|NP_000457.1|pPEX1| peroxisome biogenesis factor 1 >gi|2655141 (AF026086) (8e-80)
Putative function	Putative member of the AAA protein family (ATPases associated with diverse cellular activities) including homologies to transitional endoplasmic reticulum atpases, and an E.coli membrane-bound AAA-type metalloprotease which degrades degrades sigma32, an alternative sigma factor for heat shock promoters
Confirmation by RNAi	Slight loss of G1, increase in G2/M indicating arrest in G2/M

Line ID 238/44
Category Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/18)
Reversion R
Map Position 70D

Rescue ID F8E
Rescue Sequence
GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC
TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG
TCTTCGCTCCATTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT
GATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG
CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG
GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG
ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATTTGCCCCG
TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTATGTCTGCACGA
GAATGATCTGGTCAAAGTGTGCGCT

Other results same as for line 238/37

Line ID 428/5
Category Meiotic defects in testis: cytokinesis defects, segregation defects (seg-01/01)
Reversion ?
Map Position 70A

Rescue ID G4E
Rescue Sequence
GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGGAGCAACTTTGTT
CTGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAG
GTCTTCGCTCCATTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTC
TGATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG
CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG
GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG
ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG
TACCTCGTACCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAA
AATGATCTGGTCAAGTGTGCGCTCATCGCTGACATTCTCAACCTGCGCA

Other results same as for line 238/37

Line ID 848/7
Category Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects
Polyploidy, no overcondensation
PI-01/10
Reversion R
Map Position 70D1-2

Rescue ID G1E
Rescue Sequence 1
GGCCACCTTAAAAGTGCGTTTGAACATTCTCGTCGTGGGCGTGTGCGAATTTA
GTACGCTCCTTCCTGGTTTAAATCATTTTCGCACTAAACTTCTGCTCTCAGCGG
AATTTACTTTTGCTTTATTAGAGATGGGAGCTCGCGCATCAGCTGAGCCGATA
CTTGCGCAACAGGTGATACAGCTGATTAGAGATGGCCCTTTTCAACTGTTCCC
AGCAGTGACCGCTGCCATAACCGTTTTTCAAATTTACGTGAGAACAGACATAA
AATAAATATTACAGCTCGTAGTAAATGTTATTCTATATTTAAAAGGAAATTGT
AATAGTTAAAACTTGCAATGAATCAGTTACGTTCAAAAAAGGAAACACACTTT
AGTTTTTGGCTAGTTTATTGGGTTAATAATATTTTATTTAAAATAGTTCGAGTG
TTCAATATAGTCATGTAAATGTGTACAGAAAGATCCGGCATTTGATATTTAAT
ATATCGATTTCCCTTCACTTTCGCTCCTCGTATACCATGCTGGGGTCTTATCAA
ATTTATT

Rescue ID G1P
Rescue Sequence 2
AAGGTGGCCTATCGGCCCATCAGGAAGCAACTTTGTTCTGCTGCCGGATCAGT
ACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGGTCTTCGCTCCATTCAA
ATTAGATACGCCAAAGATTAATCCGGTCAACCATTCTGATTAGGACACGGGCT
GCCTGAGCTTGCAGTACAATGGTCGGACGCACTACGCCTCCTGGGCGCCACAA
AAGGGCGGCGGCGGCATTAAAGACACCGAGATTGGGATCAATGCCACAGCGG
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TGTGCCGTAATATTGGACTCCGGCCATCTGCCCCGTACCTCGTACGCTAGCAG
CACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAAAAATGATCTGGTCAAG
TGTGCGCCTCATCGCTGACGTTCTCAACCTGCACAGCGTCCACGTTACCCCCGT
CTCGTCCAA

Other results same as for line 238/37

Example 37 (Category 4)

Line ID	252/40
Category	Meiotic defects in testis: segregation defects, abnormal spindles. (Ab-03/30)
Reversion	R
Map Position	84E

Rescue ID A4B
Rescue Sequence 1
TACATGACTCTGCGATTTGACAAAAACAAAATTGAGTTTTGTCAAGAAAATCA
ACTATTTTTCTGTGTTTAAAAAACCGAAGCCAACAAATCCGACCAAAATGCCT
GCCGAAAACTTGGAGGAGCAGGGTCTGGAGAAGAACCCGAACCTGGAGCTGG
CCCAGACGAAGTTCCTGCTTACCCTGGCGGAATACAAGCAGGATGCGGCATTG
AAGGCGAAGCTTCTGGAGGCGATTCGCACGGAGAATATGGCCCCGTGGGTAC
GAGCACATCCTGCTCCGGAACTCGGCTTGGACCCGTTAGACAAGGATCTTGCC
TGGCGCCGAATTGAAGGAAAAACAATCGCGTTTAAGTTGGGAGCCA

Rescue ID A4E
Rescue Sequence 2
GTCATGTACTACCAGTGTGACCCCAAAGTTATCGATAAATTATACCGCATATT
TTAACATTGCCAAAAATACCAGAGCGATGTCCATCAAGATAGCGACGAAATT
AGAACAGTGCAATTGCCAATTGGGAATTTGTATTTTAATTTATTTTTAAATTCT
GAAAGTAATTTTAATTTAAAAAAAACTTGAGAGCTGTCTAGAAAAGAACTTAT
GTTTCATGATAACTTTGTCGAAGAATTAAGAAATATTTAGTTGTAAAATAATT
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Genomic hit, Accession No. AC006494

Associated ORF
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EYLCRIGDKAAAETAFRKTYEKTVSLGHRLDIVFHLIRLGLFYLDHDLITRNIDKA
KYLIEEGGDWDRRNRLKVYQGVYSVAVRDFKAAATFFLDTVSTFTSYELMDYPT
FVRYTVYYVAMIALPRNELRDKVIKGSEIQEVLHGLPDVKQFLFSLYNCQYENFYV
HLAGVEKQLRLDYLIHPHYRYYVREMRILGYTQLLESYRSLTLQYMAESFGVTVE
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SRVINI

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agctagatgcggcaatcgaggatgcggagaagaatctgggcgagatggaagtgcgcgaggcgaatcttaagaagtcagagta
cttgtgccgcatcggcgacaaggctgccgcagagactgccttccgcaagacctacgagaagaccgtttccctgggtcaccgcct
ggacatcgtgttccatctgatccgcttgggactgttttaccttgaccacgatctcatcactcgcaacatcgacaaggccaagtatctg
atcgaggaaggcggcgattgggaccgacgcaaccggttgaaggtctaccagggtgtttactcggtggcggtgcgtgacttcaag
gcggcggccacgttcttcctggacaccgtaagcaccttcacctcatacgaactgatggactaccccaccttcgtgcgttacaccgtt
tacgtggccatgattgccctgccgcgcaatgagctgcgcgacaaagtgatcaagggctccgaaatccaggaggtgctccatggc
ctgcccgacgtgaaacagttcctgttttccttgtacaactgccaatatgagaacttctacgtacacctggccggcgtagagaagcaa
ttgcgcttggactacctcattcatccccactaccgctactacgtgcgcgagatgcgcattctgggctacacccagttgctggagtcg
tatcgctccctcaccctgcagtatatggccgagtcgttcggcgtaacagtggaatacattgaccaggagctggcacgcttcatcgc
cgccggacggctgcatgccaaggtggatcgcgttggcggcattgtggagaccaatcggcctgacaacaagaactggcagtacc
aggcgaccatcaagcagggcgatctgctgctcaaccgcatccagaagttgagccgcgtgataaacatctaa

***Drosophila* Gene Hit**	BLASTN with rescue sequence 1 and TBLASTN with ORF1: 26S proteasome regulatory complex subunit p42A (AF145308).
Human Homologue	BLASTX with ESTand TBLASTN with ORF1: Hypothetical protein KIAA0107 (D14663).
***Drosophila* EST**	several including GH17651 (AI387197)

Annotated *Drosophila* genome genomic segment	AE003739
Annotated *Drosophila* genome Complete gene candidate	CG5378 - Rpn7 19S proteasome regulatory particle, non-ATPase protein, subunit S10aHuman Homologue
Human homologue of Complete gene candidate	gi7661914 8843E6684AE91ACD |ref|NP_055629.1| KIAA0107 gene product [Homo sapiens] (3.40E-149)

Putative function component of the 19S proteasome regulatory particle

Confirmation by RNAi Marked decrease in G1 and G2/M indicating fewer cycling cells

Example 38 (Category 4)

Line ID	277/7
Category	Mitotic defects in brain: anaphase defects (weak, higher condensation, some polyploidy, fewer anaphases, polyploids with monopolar spindles)
Reversion	?
Map Position	71B

Rescue ID B8E

Rescue Sequence

AGTCGGCGCATGCGGAGAGAGAATCGAAAGAGAAAGAGAAGCAAAGAGAGC
GACATACAGCAAAAACAATTCAAAAAGAACTGGTGAAGAATACGAAAATAAG
ATAATTTTTTAAGGAAGTCGCGCTTTGATCCGTATCCGTTTTAGCGTCCAAGAT
TTATATCTTAAATCGGACCTATATTTTGAGGTACAGTGAAGCTTTGATGCGCCA
GTCTTATATGAGTTAAAGTTTTAACGATTGAAAGACACCCCTGAGCTGCTCAT
TATATTTCAATATTTATAAACAATCTTATATCAGAGCTTGAGAGACTTGCATGC
GCCACAAAATTCCAATTCCAATTCCAATTCCGGAATAATTTCACAATAATCTC
AATTAACATACGTATTTTATGTTCGTAATTTTTTAAAATTCCCAGATTCCCCAC
AATTGCCATAATAATCTCGATTATGTTATTATACTCTGAGAAGTAGGAGTGTG
TGCAAAGACCACAAACAAATCATTAGGGGCGT

Annotated *Drosophila* genome genomic segment AE003584
Annotated *Drosophila* genome Complete gene candidate CG15383 – novel

Human homologue of Complete gene candidate none

Putative function No homologies to indicate function

Confirmation by RNAi Slightly increased G1 decreased G2/M indicating arrst in G1

Example 39 (Category 4)

Line ID 284/4
Category Mitotic defects in brain: anaphase defects (overcondensation, polyplody (with overcondensation), few anaphases, metaphase with bipolar spindle)
Meiotic
Reversion NR
Map Position 89B

Rescue ID 2C6E
Rescue Sequence
GTCTACCACTAGCTCTTTGTCTTCGCCTTCTAGTCTCTCTCATCTTGGCAGCCC
GTTCTAGTGCGCGTATTTTTAGTCGCAACACATTGCCCAATTCGCCAGCCGCTA
TTTGTGTCGTCCATTTGTTCATTCATCGGGCTCTTTTTCCGATTTCAGTGGGTGG
CATTTAACAATAATCCCTGCGTTCGCTGTCCACGTCCACATTACGATACGTTTA
GTGCACGGAAAGAAATAAGCGTGTGGTTTCATAATATTAGCTATTGAAAAAA
GTTCTTAAATTTAAGCCTCACTCGATTCTGATGCATGAAATATTATTGGATTGT
AAATGAGCGTCATGTTTTGGTATACAAATCTCAAAGTAATTTAAAAATTCTCA
TCTTACCGTACCTTGAACCACTACCAATCATCTCAGTACAGCATTTCAGCGAA
TTTCTCACTGTGCACTACAATGCCAGGCGGTACAAGCACCTGTATTTATTTATG
GTCCGCTGCCGTAATCGACTGCAGTCGCCGCTTCCCTCTCTCTTTGCTACCAA
CAACTTGGGGTAGGGCACCTGAACTAGTTTCAAACGGCGGCGGTCGGCCTTTT
CAGCTTTTTCGCATTTGCCATTTTCCCGCGG

Annotated *Drosophila* genome genomic segment AE003711
Annotated *Drosophila* genome Complete gene candidate CG4275 - mor transcription factor involved in chromatin remodelling

Human homologue of Complete gene candidate CG4275- 4507081 |ref|NP_003066.1|pSMARCC 2| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2(aa)

Putative function Transcription factor, regulator of chromatin

Confirmation by RNAi Decrease in G1 and G2/M and increase in polyploidy

Example 40 (Category 4)

Line ID	407/8
Category	Meiotic defects in testis: cytokinesis defects
Reversion	?
Map Position	64B1-2

Rescue ID A9E

Rescue Sequence

GACTCACCCTTTCACGCATTTCATTGGAACGTTTGTTTTCGTTTATGCACACGC
GTGTTGACACTTTTCATGAAACGCAGTGCGTGAAAAGTGCATCGCATAAACGC
AATAAATGTTTGATGGATGCGTTCTGATGGCTTGAAGTCGCCTATTTGGCCGA
TTTTCGCACGTCCACTCCCGACGGCAACAGAGTCCTGACTGAATCCCGGAGCG
GAAGGAGTGTGGATAGCCAGGACTGCCAAAGGACACTGCGCACTTTTACTTTT
TCGAAAGCGAAAGCGAAAGTGGTGGGGCCCAGGCCAAAACAANCCCTTGAGT
TGAAATTGGAAAAAAACCGGGACAGGGATGGGAGCCCAGCTCCAACAAACG
GTTCCGGATTCCTTGGGAAAGCCACGCCCTGCGCCTGGAAAAGGAATGCCCTC
CACCTCATTTGTCCTCCGTTTTGCGCTATCTCTCCCCCAAATTTCCGTTAAATG
AAAAACAACTTTGGGTTTTTGGTTTTAACAATTTCTCCCCATTTGGTTTTNGGG
TTTCCCTTTCCATTTTTGGAATTGGTTTTAATTAAAT

Genomic hit, Accession No. AC005814 64A6-64B6

Associated ORF

Genscan ORF1 predicted sequences >22:57:22|GENSCAN_predicted_peptide_2|524_aa
MGRRKDKPRVIPEQDARICRAICLCQLTMVLSCVSIVYLSVAIYSPSLKAFKSGFEL
DPVMCQTVDRQMPNNCPWASCGEWCLTKTSGFCPQIHSIVRRNGTDIQLNNCTR
VTNTSCAMIDLSRLNKFNCNNGTACNNIRGVFNCSNGHCKNMSEFFLCHHKADG
LTVNSQKDNTKLNGFFECHGVHCTKIKKPFSCDRYCSKITTTNVNTLIMHEDNLIA
ADCENAVAFNQARGSEHGVRIEPFEFWKEDDGNLLTNCATVTRESDNRITATDCI
NGTLLEHDTLPAPFMNFTQFWAIYENSTRSVDPEQRYLPNQANLTIYSWKKLFINL
EGCVNTLRGECKDFVARYGNDGDNNTAQSRYQCYYNKDSNVEFVVARYDLDK
VYRELLVSLIVPIVLFVISSISLCIITKSVKVGDDAKMRCVCAGDDSDNDGPFGPGL
ANKQQDQMYDTDDDVVDLEHQAVDGQELSDHGLPLDNQELIGSTKSLIPISPVGE
SGTSDQIFDQDQEKATTCDVPEKPLVIL

>22:57:22|GENSCAN_predicted_CDS_2|1575_bp
atggggcggcgcaaggacaaaccgcgggtgattcccgaacaggatgcgcgcatctgtcgcgccatctgcctgtgccagctgac
catggtgctgtcctgcgtgtccatcgtctacctaagcgtggccatctactcgccctccctaaaggccttcaagtccggcttcgagct
ggatcccgtcatgtgccagacggtggatcgccagatgcccaacaactgcccctgggcatcctgcggcgagtggtgcctgacca
agaccagtggcttttgcccccagatccactcaatagtgcgtcgcaacggcaccgatatccagctgaacaactgcaccagagtcac
caacacatcgtgcgccatgattgacctgagtcggctgaacaagttcaattgcaacaacggcaccgcctgcaacaatatcagaggc
gtcttcaactgctccaatggacactgcaagaatatgtcggagttcttcttgtgtcaccacaaagccgatggacttacggtcaattcgc
agaaggataacaccaagctgaatggattcttcgagtgtcacggggtgcactgcaccaagatcaagaagcccttcagctgcgatcg
ctactgttccaagataacaactaccaatgtgaacacccttattatgcacgaggataatcttattgccgccgattgtgagaacgcagtg
gctttcaaccaagcccgaggatccgagcacggtgtgcgtatcgaaccctttgagttttggaaagaggatgatggcaacctgctga

ccaactgcgccacagtcacaagagagtcggacaatcgcatcactgccacggactgcataaatggaaccctcctggaacatgaca ccttgcccgctcccttcatgaacttcacccagttttgggccatctatgagaacagcaccaggtcggtggatcccgagcagaggtac ctgcccaaccaggccaacctgaccatctacagctggaagaaactgttcatcaacctggagggctgcgtgaacacactgcgtggg gagtgcaaggactttgtggctcgctatggcaacgatggcgataacaacaccgcccagtcacgctaccagtgctactataacaagg actcgaatgtggagtttgtggttgcacgctacgatttggacaaggtttacagggagcttctagtctcgctgattgtgcccattgtgctc tttgtgatctcatctatatcgttatgtatcatcaccaaatccgtcaaggtgggtgacgatgccaagatgcgctgtgtttgtgccggcga tgattcagataatgatggcccctttggcccaggactagcaaacaagcagcaggatcagatgtacgatacagacgacgatgtagtt gacctggagcaccaagcggtggatggtcaagaactatcggaccacggacttccgctggacaaccaagagctaatcggtagcac caagtcgttgataccaatcagtcccgtcggagaatccggaactagtgatcaaatctttgaccaggatcaggagaaagcaactacgt gcgatgttcccgagaaaccactagtcatactataa

(corresponds to CG15003)

Annotated *Drosophila* genome genomic segment AE003480
Annotated *Drosophila* genome Complete gene candidate CG15003- novel unknown

Human homologue of Complete gene candidate none

Putative function No homologies to suggest function

Confirmation by RNAi Only wild type profiles observed

Example 41 (Category 4)

Line ID	422/28
Category	Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/22)
Reversion	NR
Map Position	68E

Rescue ID	2I4E

Rescue Sequence

TCGTGGACCCTCAAAGNAACGGATTTCTCCAGTTTCTTCAAAGGGTTAATAAA
CTTTTCGCACGTTTCGCATTTTTATGCTCAATCCGGTTACAAAATGCTGATAAA
ACCACTTGAACTACACGTTTCCGTACTGATAAGGGCTTTTCTTCTTATCTGACC
TCTGGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATACGCC
TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCA
CTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATT
CAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT
TGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTT
TTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTA
AAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCT
CAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAA

Genomic hit, Accession No. CSC:AC014962

Annotated *Drosophila* genome genomic segment	AE003543
Annotated *Drosophila* genome Complete gene candidate	CG5684 (putative transcription factor, human homolog
Human homologue of Complete gene candidate	1e-100 4758946 ref|NP_004770.1|pPOP2| POP2 (yeast homolog) >gi|4106061|gb|AAD02685| (AF053318) CCR4-associated regulator of polymerase II transcription

Putative function Transcription factor

Example 42 (Category 4)

Line ID 422/5
Category Meiotic defects in testis: segregation defects, abnormal spindles (Ab-04/26)
Reversion ?
Map Position 82D

Rescue ID B9E
Rescue Sequence 1
ATTGGCTCTTGATGGACTACAACGCTACCAAAATGGGGCTTGAGTTGAATTACCTGTTGGAAGACACAATGCCACCCACGATCAACAATTCGGCGGTAAACAGTGCCGCCGAAAAGCGACCCAGCGGCAAACGGGAGCGCAAGTAAGTGAACAGATCCCTAAACAGACCCAGATACTCAGACTGATGTGTACCTTGCAGATCCGAGATCATTTGCCGCGTGAAGTATGGAAACAACCTGCCGGATATACCATTTGATCTGAAGTTTCTGCAGTACCCCTTCGACAGCCACCGCTTCGTGCAGTACAACCCAACGTCGCTAGAGCGTAACTTCAAGTATGACGTGCTGACGGAACACGATTTGGGTGTCACGGTGGGACCTGATTAACCGGGAGCTCTATCAGGCCGACTCCATGACGCTGCTGGACCCGCCGATGAAAAACTGCTGGAGGAGGAGACTCTGACGCCCACAGACTCTGTGCGTTCGCGCCAGCATTCGAGGACGGTGTCATGGTTGCGCAAATCCGAGT

Rescue ID B9B
Rescue Sequence 2
GGCCAAATCTAGAAATCCTCAAATCTGCGCTTGGCAGTGTGACCGTACTTGACCGGTACGATAATACCTCCGGTAAAAAAAATACTATATTTCCGGGGGACTCAAATGCAACATCCTCATCGTATATAACACAACATCTATTTGAATTTCATTTCCACAACTAATATTATGGATAATGCTTTATTATCATTTTCCAAGTTAGCGATAAATCACCCCACAAGCTGAAAAATCAACGTTTAAAAACGATTGATATTTTTTTTAATACTTTTTGGTTTTACTATTTGAATTTTTGTATACTTTTAGATTTTACTATTTTAATTTTTCGTTTCTTCTAGCTGACTAACGGGTTAAAAAGGATCCGTCGACCTGCAGATCTCTAGAAGCTTGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCCGTGCGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCCTTCT

Genomic hit, Accession No. AC008189
Associated ORF
Genscan ORF1 predicted sequences >15:53:24|GENSCAN_predicted_peptide_3|211_aa
MRNANESSGKPKSKFVSNEFHALFSTICSIADSPAVSREKLKIDLAARKIPSASAPKGDSPLERFSRDLFTYLRSVCRWGRFSAALFTAELLIVGGIVSSNRTSESSETGNPLANEPDPLYMKLVDPMVAGESPKRMIKDQKDVGLKSTSSSEELRKLPKTRGRQKRFIRNPNYVKANEFYDKMLSSEYVSKRYKDLPPPHPGFGADQPPA

>15:53:24|GENSCAN_predicted_CDS_3|636_bp
atgcgcaacgcaaatgaatcgagcggtaaaccaaaatcgaaatttgtaagcaacgaattccacgcattgttttcaacaatttgttcaa

ttgccgattccccggctgtctctcgagaaaaattgaaaatcgatttagctgctcggaaaataccttcggcatcagcccccaaaggg gattctccactcgagcgcttttcgcgggatctgttcacttacttgcgctccgtttgccgctggggtcgcttttcggcggcactgtttacc gccgaattgttgatcgtgggtggcattgtgtcttccaacagaacgtcagagtcttctgaaactggaaacccacttgcaaacgagccc gatccattatatatgaaactggtggatcccatggtagcaggagaatcacctaaaaggatgattaaggatcagaaagatgtaggcctt aaatcaactagcagtagcgaagagctccgaaaattgccaaaaacgcgaggtcgacagaagagattcattcggaatccaaactat gtgaaagctaacgaattctatgataagatgttaagcagtgaatacgtaagtaagcggtataaggatcttccgccgcctcatccggga tttggagcggatcaaccgccagcatga

Corresponds to CG2503

Annotated *Drosophila* genome genomic segment	AE003605
Annotated *Drosophila* genome Complete gene candidate	CG2503 - novel possibly RNA binding
Human homologue of Complete gene candidate	3287674 AC005239 (AC005239) F23149_1(aa)

Putative function Possible RNA binding protein

Confirmation by RNAi Almost no G1 and broadened G2/M indicating arrest in G2/M

Example 43 (Category 4)

Line ID	423/14
Category	Meiotic defects in testis: cytokinesis defects,abnormal spindles (Ab-16/13)
Reversion	R
Map Position	67B1-10

Rescue ID E9E

Rescue Sequence

GTTTGGCGTAAAAGCTTCGGCTGTGTTTGGTGCCCAAAATTTTCCACTGCTTCT
CTTTTTGTGTATCTCTTATATCTTGTGCTTTTTTGTTGTGTATGTTTTCTCGTTTC
TTTTTGCACACGCGCTTCGCGTTGCGGGCCAGCTGTTTTTGTTTGATAAGTGGT
TACGGTTTGTGTGTGCCAGCGGGTTTTCCTTAGTCGAACTGCTCGCGATGACTG
ATTTTTCACAAGTGACTCAAAAACAGTCGATCGCCCTTTTAAGAAAACCCGCT
CAACGCACACAAAAGCGGTTTCTCTCTTTTTGTCGTTCTCTCTTTTCACACTGA
CCACACGGAACGAAAAAATGATTACCGACCACACGGAAAGAAAAATTTATGT
CCAGACGAAACTATTTTTGTCCAACTAGCTGATTTGCATAACAATTTAAGCCA
CAAGAAACTAGATTAAAATTTTACATTTAAATACATTATCAAATCCGAAATAT
CAATAATTGTAATTTATCCTTACAAAATGTTA

Genomic hit, Accession No. CSC:AC020214
***Drosophila* EST** several including LP12306 (AI297868)

Annotated *Drosophila* genome genomic segment AE003552
Annotated *Drosophila* genome Complete gene candidate CG3967 - novel

Human homologue of Complete gene candidate none

Putative function No homologies to indicate function

Confirmation by RNAi **Only wild type profiles observed**

Example 44 (Category 4)

Line ID	427/5
Category	Mitotic defects in brain: anaphase defects. Meiotic defects in testis: segregation defects, abnormal spindles (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20)
Reversion	?
Map Position	67B1-5
Rescue ID	H4E

Rescue Sequence
GTACAGCCTGAAGTGATCGTTGTTGTTTGAATCGGTGCTATCGGCGGTTGCGC
TTTGTGGGCATCTTTATCCAATTTGCTATGCGCGCTTGTCCTTAAATTTTGAAC
TGTATTCCAAGGGTTGCTTTGGCGGCTATCGATAGTATCGGCATGGTTACATTT
TAGTTTTATAACAAGAATTTTACAGGTATTTTGATTATCTGAGCTTAGTTTTAA
GCAANAATATTATTGTTAAAAATTTAAAAAGTAAACAAGCTATTTTAACAAGC
ATTTAAACAAATAGTATTAATAATATAAAAATATATCGATATGTGTTGCAAAT
GTTCGTTCCCTTAGTATTCTCTCATATTTATTTCAAATAAACTGTATAAAATAT
CTGAAAAAGCGAACATATTTATTTAATTTCATCGCAGATATCGATATCACAGC
GCTGCTATCGATGGTGTGTCTGTCGCAGTGCCTATCGCTTACCCTGCCATCGCT
AACAAAAA

Genomic hit, Accession No. CSC:AC020120

Associated ORF
Genscan: ORF2 predicted sequences >22:06:07|GENSCAN_predicted_peptide_7|464_aa
MPSEQHTNIKVAVRVRPYNVRELEQKQRSIIKVMDRSALLFDPDEEDDEFFFQGA
KQPYRDITKRMNKKLTMEFDRVFDIDNSNQDLFEECTAPLVDAVLNGYNCSVFV
YGATGAGKTFTMLGSEAHPGLTYLTMQDLFDKIQAQSDVRKFDVGVSYLEVYNE
HVMNLLTKSGPLKLREDNNGVVVSGLCLTPIYSAEELLRMLMLGNSHRTQHPTD
ANAESSRSHAIFQVHIRITERKTDTKRTVKLSMIDLAGSERAASTKGIGVRFKEGAS
INKSLLALGNCINKLADGLKHIPYRDSNLTRILKDSLGGNCRTLMVANVSMSSLTY
EDTYNTLKYASRAKKIRTTLKQNVLKSKMPTEFYVKKIDEVVAENERLKERNKA
LEAKATQLERAGNSGFDPLELKTWYSKIDAVYAAARQLQEHVLGMRSKIKNINY
RQTLKKELEEFRKLMCVDQRVCQESF

>22:06:07|GENSCAN_predicted_CDS_7|1395_bp
atgccttcggaacagcatacgaatataaaagtggcggttcgcgtacggccgtataatgtccgtgaattggagcaaaaacagcgga
gtattatcaaggtcatggatcgttcggcactgctgttcgatcccgacgaggaggacgatgagttcttctttcagggcgccaagcaac
cgtaccgcgacatcaccaagcggatgaacaaaaagttgaccatggaattcgacagggtattcgatatagacaattccaaccagga
tctgttcgaggagtgcacggcgccgctggtcgacgcggtgttaaatggatacaactgctcggtatttgtatatggagccactggcg
ccggaaaaacattcacaatgctgggcagcgaggctcatccgggtctgacctatcttaccatgcaagatctcttcgataagatccaa
gcgcagagcgacgtgcgcaagttcgatgtgggggtatcctatctagaggtgtacaacgaacatgtgatgaatctgctaactaaatc
gggcccctttaaaacttcgcgaggacaacaatggcgtggtggtcagtggtctttgtctcacgcccatctacagtgccgaggagctgc
taagaatgctgatgctgggcaactctcatcgcactcagcacccccacagatgccaatgcagagagttccaggtcacatgccatcttc
caggtgcacattaggatcacggagcgcaagaccgacaccaaaagaacggtcaaactatccatgatcgatctggcgggcagtga
gagggcggccagtacgaaaggcattggagtgcgattcaaggaaggcgccagcatcaacaaaagtctcttagctttgggaaattg

cataaacaagctagccgacggcttaaagcacatcccgtaccgcgactcgaacctgacacgcatcctgaaggactcgttgggcgg aaattgtcgcacattgatggtggccaatgtctcgatgagctcactgacctatgaagatacctacaacacccttaagtacgctagccg agctaagaagatacgcacgactctgaaacagaatgtcctcaagtccaagatgccaaccgagttctatgtgaagaagatcgacgag gtggtagccgagaacgagcgactcaaagagcgcaacaaggcgctggaggccaaggccactcagttggagcgcgccggcaat agtggattcgatccgctggagcttaagacgtggtacagcaagatagacgctgtatatgcggccgccccggcagcttcaggagcac gtccttggtatgcgtagcaagatcaagaacatcaactaccggcagacactgaaaaaagaactggaggagttcaggaagctgatgt gtgtcgaccagcgagtgtgccaggagagtttttaa

***Drosophila* Gene Hit** TBLASTN with ORF2: kinesin like protein 67a (U89264)
Human Homologue TBLASTN with ORF2: kinesin family member protein KIF3A (AF041853)
***Drosophila* EST** GH22018 (AI402731)

Annotated *Drosophila* genome genomic segment AE003552
Annotated *Drosophila* genome Complete gene candidate CG10923 Klp67a - motor protein

Human homologue of Complete gene candidate 2e-58 4758646 kinesin family protein 3B >gi|3913958|sp|O15066|KF3B _HUMAN KINESIN-LIKE PROTEIN KIF3B and also predicted peptide ENSP00000166696 Gene:ENSG00000073652 Clone:AC015936 Contig:AC015936.00023 6.70E-91 (predicted kinesin?: ENST00000166696)

Putative function motor protein involved in cytoskeleton organization and biogenesis

Confirmation by RNAi Almost no G1 and broadened G2/M indicating arrest in G2/M

Example 45 (Category 4)

Line ID 442/3
Category Meiotic defects in testis: segregation defects.
Reversion ?
Map Position 70D4-7

Rescue ID H7E
Rescue Sequence
CGCAAGACTGTCTTCGATAGCAGAAGCGTTATTTCGGAACATATCGTTTATCG
AAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA
ACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT
AAAATATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAGCG
AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA
TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTTCA
ATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT
GTAACTGTTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCATC
GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA

Genomic hit, Accession No. CSC:AC017664

***Drosophila* EST** CK02287 (AA141680)

Annotated *Drosophila* genome genomic segment AE003536
Annotated *Drosophila* genome Complete gene candidate CG6650 - novel transacylase like

Human homologue of Complete gene candidate none

Putative function Transacylase

Confirmation by RNAi Marked increase in G1 indicating arrest in G1

Line ID 473/22
Category Meiotic defects in testis: no division (no meiosis)
Reversion R
Map Position 70A1-5

Rescue ID 2B7E
Rescue Sequence 1
CGCAAGACTGTCTTCGATAGCAGAAGGCGTTATTTCGGAACATATCGTTTTAT
CGAAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTC
AAACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAA
TTAAAATATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAG
CGAAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTC
TATGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTT
CAATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAA
ATGTAACTGTTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCA
TCGCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATAAGAA
AGTTGGCGTAGCCGGAAGGCGGATTGTCACATACAAAATAGTTTGGAAAGCC
CAAACTGAG

Genomic hit, Accession No. CSC:AC017664
***Drosophila* EST** LD47104 (AI515336), SD03663 (AI532240)

For other results see line 442/3

Line ID 670/6
Category Meiotic defects in testis: segregation defects, abnormal spindles (Ab-12/48)
Reversion ?
Map Position 70C

Rescue ID H7E
Rescue Sequence
CGCAAGACTGTCTTCGATAGCAGAAGCGTTATTTCGGAACATATCGTTTATCG
AAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA
ACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT
AAAATATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAGCG
AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA
TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTTCA
ATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT
GTAACTGTTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCATC
GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA

Genomic hit, Accession No. CSC:AC017664
***Drosophila* EST** CK02287 (AA141680)

For other results see line 442/3

Example 46 (Category 4)

Line ID	460/20
Category	Meiotic defects in testis: segregation defects, multipolar spindles (mitotic: High polyploids, no diploids, higher mitotic index Meiotic: Mul-02/59)
Reversion	NR
Map Position	78A1-4

Rescue ID	2B8E

Rescue Sequence

AGCTGGTCCAATTGGAAACGTTAGCTGCTCCAATGGGAGCAGCTGGCGCTCTC
TCTTCGATCGCGCTCGCTCTCATCCTCTCTCTTTAGCTTGTGCCACAGTAGCTG
CCGAAGGCAATTTTCATGTGCTCGTGTGTCGACCCCCACTCAGCCCACTTCTG
ATCGGAATCGGGGATTCGGAATCGTGTAAGGCAGCCTTTGAAGGTCCCTTTTC
CAGGTGGCGGCCGTATCCTTAAAGTAAACATAGTTCAACTGACTTGGCAGCGC
TCCAAATGCGGTGACTTCTTGGCTATGTCATATATACCCCCACTCCCCTCCTGA
CTACCCTGCCACGCCCCACCGCCCACCGTCGGCGACGACAATTCCATTAAAAG
TTGTACGTTGTCACTTTGCGTTAACTTATCTGTGGAGCATGTTGTGCGATCGCA
TTTTTATTGTCGCCATTGTCTCTCGCTCTCTCCATCGCTCTTTCGCCTGGCTTCC
CTACCCTGCCCACACAGGGAAGCCTACACACTCTTAAATCATGCACTTGGAAC
AAAAAGTGCAAGCATTAAACTTTATTTAAACATTCAAGAGCCGCTTCTCTATT
TACCATTGAAAATTTAATTTAAAATAGAAGAGGCCTTTTCAGAATAATATAAT
ACCTTTAAG

Genomic hit, Accession No. CSC:AC020460

Annotated *Drosophila* genome genomic segment	AE003592
Annotated *Drosophila* genome Complete gene candidate	CG10588 - novel gene with homology to proteases

Human homologue of Complete gene candidate	2e-74 4505453 ref|NP_002516.1|pNRD1| nardilysin (N-arginine dibasic convertase) >gi|2462488|emb|CAA6369

Putative function	Novel protease

Confirmation by RNAi	Marked increase in G1 indicating arrest in G1

Example 47 (Category 4)

Line ID	477/16
Category	Meiotic defects in testis: segregation defect.
Reversion	NR?
Map Position	90C5-10

Rescue ID C3E

Rescue Sequence 1

CTGTGGACGGTCGTCAATGCGTGAATATTCTTCTATGTGTAAGTGGTGTGCGT
GTATGTAGATTTCTGGTTAAGAAAAGCCCCAAAAACCAAAGCGCCCCGCAAA
ATATATATTGAGTCTTCTTGGCCCAACAACAAATCTGCCGCCGGACTTTCGCC
GGAGGGCGAGTGAAAAATTCAGTTTCTCTCCTCTCGACGATGCACTTTGGAGG
CTGTGTGAGTGTGTGTGCGAGTGAGTGCGTGTGTGTATACATATGCAAATGAT
TGGATGTCGAATCCTTGCATCATCATCATCTTCATAAACACTTGGCGAAAAAC
CGCAGGAAAACGCAAGCAGCCGAACAAAAAAAGAGAGCCTCTCAAGACAAC
GGCAGCGGCCAAAAGTGAACGCGCAACAAACGCGGCCAAGCAGGCGCGGCA
ATTATTTATAAATCTTAAGCCGTTAGCCCCCCTCTCTCTCCCACTCACGAAAAG
AAAATAAGTTAAACCAATTGGTGAAGATGATGCCCC

Rescue ID C3P

Rescue Sequence 2

GTCCACAGACTGGCTATATATACTAAAAACGAACTCGCGTGAGAAGACAGGG
ACAGGGCAGCAAACTCGGTATACGAACGGAACGAAATGAAACGATTCAAGTA
GTAGTGTATGCAAGTCTTGTCTGTCTGCGCCTGGCGTTCTTTTCTCTTCTTTTTT
TCGATGGTTTTTCGCCAGGCTGGGCGCTGCCAAAACGCTGATACGGCGGCCAC
AATCACACGCGGCTAATCGCCAGTTGGGCCCTGCACAGGCTGCACATACTTTT
CACTATTAATGCGCTGTATTTCACTTATTTTTCGAACAAATTCGCAGCATGACG
AAGAAGCGAGCCTGTACAAGATTAGAGCGGGTAGCACGCACGATAGTATCGA
TACGTACGAGTATTTGGCACTGCGATACATTATCGGTGCTCGTTTCGATAGCCC
CCGATAGCTCTAGCACGAAATTTTATCGCTTTATCCATATTTTATACTATTTTT
ATTTATTGGACTTCAATGAATATTTAATTTACGTCTGGGTCGCTTTTTAAATAT
ATATGGTAATCAATAGCTGGCGAATTAGCGATATTTGAGTGTGACGCAAAAAT
GAGTTGCATCGATATCGATTTCTCGCTACTCTGGGACGCCATCTTTATTGCGG

Genomic hit, Accession No. AC007810

Associated ORF

Genscan ORF1 predicted sequences >17:48:58|GENSCAN_predicted_peptide_2|349_aa
MSRILFILLLLIVTQLSELQAAAFSVRQNRFDEVPDLQTPAPLATSTESSKKPEKAT
SGLLKKCLPCSDGIRCVPQIQCPAHVRMESHEKPQICDLPAGKFGYCCETGQNHT
APKPETSPKERRSGFPTILSPAVLDEARRNFEHLMHGVAQIPVRRGFPDFAHGLVF
HSTAKDDLHNFAISNSAIEQVMTTQLFGKKEQVPVEDFITNNVPIKFTETPLAHHC
QPPPVCGNIRSVYRSMDGTCNNPEPQRSLWGAAGQPMERMLPPAYEDVPSASPA
AICSYIYGIASRLAPVSVVNCCTFAWQLDWTTGMASGECVCVECMPAEWRLGQC
PLLHEASSEMSRLLAKS

>17:48:58|GENSCAN_predicted_CDS_2|1050_bp
atgagtcgcattttatttattttgttgctacttattgtgacgcaactgagcgagttgcaggcggcagcattttctgtgcgccaaaatcgtt
ttgatgaagttcctgatttgcagactcctgcacctctggccacttccactgaatcttctaagaaacccgaaaaagctaccagtggtct
gctgaaaaaatgccttccctgcagcgatggtataagatgcgtgccccaaatccagtgtcccgcccacgttcgcatggaaagccat
gaaaagccccaaatttgcgatctcccggctggaaaattcggctactgctgcgagactggacagaatcacactgctcccaagccg
gagacctctcccaaggagcgtcgatccggatttcccaccattctgtcacccgcagttttggatgaggcgcgtcgcaatttcgagca
cttgatgcatggagttgcgcagattccggtgcgccgtggctttccagattttgcccatggcctggttttccactcgacggccaaggat
gaccttcacaacttcgccatatcgaacagtgccattgaacaagtgatgaccacccagttgtttgggaagaaggagcaggtgcccg
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aatattcggtctgtttatcgcagcatggacggcacttgcaataatccagaaccacagagatctctgtggggtgctgctggtcaaccg
atggagcgcatgctgccccccgcctatgaagatgttccgtcagcttctcctgctgctatatgtagttatatctatggcatcgcatctcg
tctggcgcctgtttctgttgtcaattgttgcacatttgcatggcaattggattggaccactggaatggcgagcggggagtgtgtgtgt
gtggaatgtatgccggcggagtggcgtttgggccaatgcccgttgcttcatgaggcgtcgagtgaaatgagccgcctcttggcta
aaagctag

***Drosophila* Gene Hit** rescue sequence: eyelid/osa (AF053091)
Human Homologue BLASTX with eyelid: KIAA1235 protein (AB033061) Brain protein 120 (AB001895)
***Drosophila* EST** several including LD04852 (AA201670), LD24466

Annotated *Drosophila* genome genomic segment AE003718
Annotated *Drosophila* genome Complete gene candidate CG7467 - osa DNA binding putatively involved in DNA packaging

Human homologue of Complete gene candidate CG7467 - 7e-25 2588991 dbj|BAA23269| (AB001895) B120 [Homo sapiens] and O14497 SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN SUBFAMILY F MEMBER 1 3e-67

Putative function transcriptional regulator

Confirmation by RNAi Only wild type profiles observed

Example 48 (Category 4)

Line ID	496/4
Category	Meiotic defects in testis: segregation defects,abnormal spindles (meiotic: Ab-08/42)
Reversion	NR
Map Position	65E4-7

Rescue ID 2C1E

Rescue Sequence

GCACGATCGCTCTCTCTTGGCTCTCTCTATCACTCTCTGGACTCTCTCTCAGCA
CCTTTGCTACCGTTTCGCAGAACAGGTGTATCGGTTTTCAAGGCAACTGTGATT
TTTTAACTCAACATTCTATATCGAAAACTTGTAGAGGTCGGAATTTTTCTTGAG
CGCCTAAAAGTGTGCAGTGAAATCATTTAATCCACTTCCGGTTGCAAAACAGG
AATCACACATATGAAGTGATTAAAAATCATAGAAGGTTTGACACCTTCAAATA
ATAAGAAAACAAAAATTTGTAAACTGTGATAATTTATTTAATTGAAATCTTAA
TTTAATGGCCTACAAATCTGTTGAATATCCGTTGAATACACTTTTCCAGGGTGT
GTCCTAGTCGGCTCCTCTTTGTTACCCCAGTTTGCTGGTCTTCTTAGCCGCACA
CCAGTTTATCGCTGTTTTGCCTTTGCGCTTTTCATTCATAAACAAAAAACAATG
TTATTGTTATTGCGGTGGCTGTAGATGTAAATGTAAATGTAGATGTAGAGGCT
GCTTCTTGGG

Genomic hit, Accession No. CSC:AC018039

Associated ORF

Genscan ORF1 predicted sequences >19:35:36|GENSCAN_predicted_peptide_6|190_aa
MVSEQFNAAAEKVKSLTKRPSDDEFLQLYALFKQASVGDNDTAKPGLLDLKGKA
KWEAWNKQKGKSSEAAQQEYITFVEGLVAKYDNGMHKQEPNTCQARNATRFR
KSSECSLDQNTYTSSVTVIPAFHEGPKNSTASWPRIYRCYQRNQQAANCKWANTN
SVCGKPHGKQSRRIIFAEFLAGHTVQILG

>19:35:36|GENSCAN_predicted_CDS_6|573_bp
atggtttccgagcaattcaacgccgccgccgagaaggtgaagagcctgaccaagcgtcccagtgatgacgagttcctgcagctg
tacgccctgttcaagcaggccagcgttggtgacaacgacaccgccaagccgggtctcctggacctgaagggcaaggccaagtg
ggaggcctggaacaagcagaagggcaagagcagcgaggccgcccagcaggagtacatcacctttgtggagggcctggtggc
caagtatgacaatggaatgcacaaacaagaaccaaacacttgccaagcacgcaatgcgactcggtttcggaaaagctcggaatg
ctcgctggatcagaatacgtatacgtccagtgtgacggttatacctgcattccacgaaggtccaaagaactcgacggcaagttggc
caagaatttaccggtgctatcagcggaaccaacaagcggccaactgcaagtgggcaaacacaaatagcgtttgcgggaaaccc
cacggaaaacagagccgccgaatcattttcgcagaatttctggccggccatacggtgcagattcttgggtaa

***Drosophila* Gene Hit**	rescue sequence: melt (S144114) P element insertion site (AF174669), TBLASTN with ORF1: diazepam binding inhibitor (DBI) (U04823) and melted (AF205831)

Annotated *Drosophila* genome genomic segment	AE003560
Annotated *Drosophila* genome Complete gene candidate	CG8624 melt - putative signal

transduction protein
CG8631 msl-3 - acyl-CoA-binding
protein/diazapam binding inhibitor

Human homologue of Complete gene candidate	CG8624- predicted gene ENSP00000065899 Gene:ENSG00000055889 Clone:AC015904 Contig:AC015904.00014 1.70E-15 (unknown predicted gene 1: ENST00000065899 and AK022666 Homo sapiens cDNA FLJ12604 fis 2e-29 CG8631- gi5803104 0C85AE40FDF874CD |ref|NP_006791.1| male-specific lethal-3 (Drosophila)-like 1 [Homo sapiens] (1.70E-36) and Ensembl predicted peptide ENSP00000006617 Gene:ENSG00000005302 Clone:AC004554 Contig:AC004554.00001 8.70E-19 (unknown predicted gene 1: ENST00000006617
Putative function	CG8624: putative signal transduction protein CG8631:acyl-CoA-binding protein/diazapam binding inhibitor
Confirmation by RNAi	CG8624: reduced G1 and G2/M Indicating fewer cycling cells, CG8631: Increased G1 to G2/M ratio indicating arrest in G1

Example 49 (Category 4)

Line ID	523/19
Category	Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02
Reversion	R
Map Position	75C1-4

Rescue ID 2B4E

Rescue Sequence

ACTGAGAGCATATTTGTGCACCAGAGGGCTGCATAACAACATTCTCTTTGTCC
ATTCGTTATACTTCGTATTCAGAATACATGTCATTCAGTTGGTCCCGTTCTTTTT
GCGTTCACTTCGTATATATTCGGCGATCGAAATGAACTAACTGAATGTGTTCA
AAGAATGAATGAAGCCAATGAATTTTCAATAGTAATTCAGAGTGCTTAAAATT
CTTCATGTTGTCATTGAGTAAAATGAGTTCGGACAGCGCGAAGGTAAGTCGAA
GTTTGTGTTTTATTATGTTTATTTGTATTATTATGTACACTAGTCGGCATACTTT
TGCGTGCGTCTTATACGTGTGCGTCTTATTTAACAATATTGTAAAATAAAATAT
ATAAATTATTTGTTATATGCGTAGGGGCCTTTATTTTGTGTATTGATAGTCTTTT
GTCATAGATATCATTATTCTGACAAGATTTGAACTTTTCAAGTTATTGCCTCTC
GTTATTCAATTCCTAGCTGGTCTTACGTTACGCGATATTTCCTAAAATATCCTA
AAATCGCACAAAACAGTCACGCCCACACTTTTGAAAAACGTGGTAATATTTTT
CATACTTGCATTAAGTCTGG

Genomic hit, Accession No. AC007691

Annotated *Drosophila* genome genomic segment	AE003520
Annotated *Drosophila* genome Complete gene candidate	CG4306 – novel
Human homologue of Complete gene candidate	4e-25 3242764 (AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens]

Putative function No homologies to indicate function

Confirmation by RNAi Only wild type profile observed

Example 50 (Category 4)

Line ID	666/19
Category	Mitotic defects in brain: anaphase defects (weak, overcondensation, aneuploidy, lagging chromosomes, metaphase with bipolar spindle)
Reversion	NR
Map Position	64E1-5

Rescue ID I9E

Rescue Sequence

CCCTCGTCTACGTCGAAATTCTGGATGCTTCTCGGATTTAGGGTTGTATCTCGA
AAACGTTTGACTGCGAATGTCAATATCGATATGCTAACCGATAGCTGTCGATG
TTTTAAACACAGTGCACTGTTTTAAATCGCTCCCCATTTATATATATTTGTGC
NTGCTTTTGGCGGTNNTTTTCTTTATATGCTTCTTATGCTTTTACGATTATTATT
AGCGCTTATTTGATTGCAAATGCCAAGGAAAGCGTGACTGTGATGGCGAAATG
CGGAAAGTACTCCTTAAATCTCATATATCGCATAAAACTATCGGTTCTGGAAT
GTTTCGTGTAAGTCTGCGAAGATAGAGATCGATCTATTTTGAGGATACATTTG
TTAATATTATAAGGGATTCTTCTACAGGGGTCAGATTGCTTAAAAACACACAG
AANAATAAACAAAATATTTCTTTGAAATATTGAAATATTTGAAATANAAAAAA
CGTATTGACGAGGTAAGCATATTGAAAAAGATAGGAAGGTGATGGAGAAAGT
GCACTTATATTGGTCACCAAAGAGCTTATAATCAAAAGATCAATAGATATAAA
TATCTTTATATGATATAAAATATAATACATATAATATAATATCATATACAATG
GATAAATTGCAAGTGGCAAAATGAATTCCGCGGAATTAATTCTGAANCGAAA
GGGCCT

Genomic hit, Accession No. CSC:AC014815

Associated ORF

Genscan ORF1 predicted sequences >17:46:43|GENSCAN_predicted_peptide_1|334_aa
MGKDFYKILGLERKASDDEIKKAYRKLALKYHPDKNKSPQAEERFKEIAEAYEVL
SDKKKRDIFDNYGEDGLKGGQPGPDGGGQPGAYTYQFHGDPRATFAQFFGSSDP
FGAFFTGGDNMFSGGQGGNTNEIFWNIGGDDMFAFNAQAPSRKRQQDPPIEHDLF
VSLEEVDKGCIKKMKISRMATGSNGPYKEEKVLRITVKPGWKAGTKITFPQEGDS
APNKTPADIVFIIRDKPHSLFKREGIDLKYTAQISLKQALCGALVSVPTLQGSRIQV
NPNHEIIKPTTTRRINGLGLPVPKEPSRRGDLIVSFDIKFPDTLAPSLQNQLSELLPN

>17:46:43|GENSCAN_predicted_CDS_1|1005_bp
atgggcaaagacttctacaagattctgggcctcgagcgcaaggccagcgacgatgagatcaagaaggcctaccgcaaactggc
actcaaataccatcccgacaagaacaagagcccacaggcggaggagcgcttcaaggagatcgccgaggcgtacgaggtgctg
tcggacaaaaagaagcgcgacatcttcgacaattacggtgaggatggattgaagggcggacagccgggaccagatggcggcg
gtcagccgggagcgtacacttaccagttccacggcgatccgagggccacatttgcccagttctttggatcgtcggatccgtttggc
gcgttctttaccggcggcgataacatgtttagtggcggtcagggcggcaataccaacgagatcttctggaacattggcggcgacg
atatgtttgcctttaatgcccaggcacccagtcgcaagcgccagcaggatccgcccatcgagcatgatctgttcgtgtcgctggag
gaagtggacaagggatgcatcaagaagatgaaaatctcacgcatggccaccggaagcaatgggccgtacaaggaggagaag
gtgctgaggatcacagtgaagccgggctggaaggccggtaccaagattaccttcccccaagagggtgattcggcgccaaacaa

gacgccagctgacatcgtcttcatcattcgcgacaaaccgcattcgctgttcaaacgcgagggaatcgatctaaagtatacagccc agatcagtctgaagcaggccttgtgcggagcactggttagtgtgcccacgctgcagggcagcaggatacaggtgaatccgaacc acgagatcatcaagcccaccacaacgcgccggatcaacggactgggtctgccggtgcccaaggagccatcgaggcgcggcg atctgatcgtctccttcgacattaagtttcccgacacactggcacccagtctgcagaatcagctgtccgagctgctgcccaactag

***Drosophila* Gene Hit**	rescue sequence: fasciclin I (FasI) (M32311) TBLASTN with ORF1: DnaJ homolog (DROJ1) (U34904)
Human Homologue	TBLASTN with ORF1: DnaJ-like heat shock protein 40 (HLJ1) (U40992.2)

Annotated *Drosophila* genome genomic segment	AE003565
Annotated *Drosophila* genome Complete gene candidate	CG10578 - DnaJ-1 a chaperone putatively involved in protein folding. Stimulates activity of HSP70
Human homologue of Complete gene candidate	8e-94 1706473 P25685 DNJ1_HUMAN DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40)

Putative function Chaperone involved in protein folding

Confirmation by RNAi Almost no G1 peak, increased G2/M indicating G2/M arrest

Example 51 (Category 4)

Line ID	714/11
Category	Meiotic defects in testis: cytokinesis defects,abnormal spindles (Ab-01/04)
Reversion	?
Map Position	66A10-15

Rescue ID 2A4E
Rescue Sequence
AACCAGAACGAAACTCCAATGCAGTTTCATTTTGTCAGTTTAATCATTAAACA
AAGAACTGCGCAACCGATCGCAACTAGCTCGTGGACTCTTGTTCTCCCAATAA
TTGGTATGTTTTCCATTTTGCGTTAACATGGAAAATGTGTGAAAAGCTTTTTCC
CCCTCCAAAAGAAGCGTACTGAACTAAGCTTTCGGTGGTTAGTAATAGTAGTC
GTTATATCTTATTTTTCTTATTTACGTGCAGCTGCAATCATTGGCTGCGTCACTT
TGGCGTCAGCTATAAACTGGTGGATCAACTCGGCGGCCTCCAAAAGCTGCGCA
TCTGCTCCAGACACTTTAGCCAACGCCAGGAGATGGCCAAAACCCGCATCAA
GATGACGCCGCTGCGCAAGTCCTCGTCCTCCAAGGGCATTGTGCTACCCATTA
ATGCCGCTGGAGGGTCGGTCATTGCAGGCGCCTTAGCACGAGGAGGAGGTGC
A

Genomic hit, Accession No. AC012390

Associated ORF
Genscan ORF1 predicted sequences >19:47:45|GENSCAN_predicted_peptide_2|711_aa
MRSHQAVGNLLLAADEALPAVQSASVYVVWMAEQPLSPGQSYDIKIADSPSVSS
KSITDNGADVQWFAFEHSQYYQGVQQMFLSALERIDSEFLITLIKRCPYHVDSLVQ
LSEVCKMTEDFSLASELLERALLLLESSLHINFSLTSGNCRLDYRRQENRSFYIVLF
KHAQYLEERACSRTAFEISKLLLSLQPDTDPLAMILPNQPDQCTGNMTQLQQAGK
IRKRSEKQFPIGTEPRGTDALRFTLQTLASAGRDITWNIKRLQGSRVTGAAQGYLI
DKKTAVQYKITIIAHLKDPNIDQLFDSSGDGKADLHGSTPDWGCQAMMADAISR
YKEGNPVFYYTWTPYWVSNELKPGKDVVWLQVPFSALPGDKNADTKLPNAGGI
EGLIADEEVQVLDALCDAPCVGVSHSCRLLDGNRRGNNELRLFIPGKSQFGVADG
CADKQSVMEYHAAKTGHTKFSESEEEKKALTEEEKKAQLALIEEKLKQKRIEREE
REKIEALQREKNRIKSGKDMTEAKRRMEELEMKKIVEQRKREKDEEKAARDRVK
AQIEADKAARKAREQKELGNAEPAPSVSSTTVSSPPAGVKSPPRDYTETRIQGASA
ILAAAAPYYQPPAVPQDVQPDRPIGYGAFGVVCGSHISGWHCSAGHYEDGNENFE
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>19:47:45|GENSCAN_predicted_CDS_2|2136_bp
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acagataatggagcggacgttcaatggtttgcctttgagcatagccaatactaccagggagtgcagcaaatgttcctttctgctctcg
agcgcattgactcggaatttctgatcacacttatcaaacgctgcccctatcatgtcgactccttggttcaactcagcgaagtatgcaa
gatgaccgaagacttttccttggcctccgaactgcttgagcgcgcccttctccttctggaatcgtcgctgcacatcaacttcagtttga
cgtcgggcaactgccgactggactaccggagacaggaaaaccgatccttctacatcgtgctgttcaagcacgcgcagtacctgg

aggaacgagcttgcagccgcaccgccttcgagatctccaaactgctcctgagtcttcagccagacacagatcctcttgccatgatt
ctaccaaatcagccggatcaatgtaccggcaatatgacgcagctgcagcaggcgggcaaaatccgtaagcgctcagaaaagca
gtttccgatcggtactgaaccgcgcggtactgacgcgttgcgcttcaccctgcagacactggcgtctgccggtcgcgacatcacct
ggaatataaagcgtctgcaaggttcccgtgttaccggcgcggcccagggttacctcatcgataagaaaaccgccgtccagtacaa
aatcaccatcatcgctcatctgaaagatccgaatatcgaccaactgttcgattcaagcggcgacggaaaagcggatttacacggta
gtaccccagactggggctgccaagctatgatggccgacgccatcagtcgctacaaagagggcaacccggtgttttattacacctg
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cccggcaaatcccagtttggagtagctgatggatgtgcagacaagcagagtgttatggagtaccatgccgccaaaaccggtcac
accaaattctccgaatcggaggaggaaaagaaggcgctcaccgaggaggagaagaaggcccagctggccctcatcgaggag
aagctcaagcagaaacgcatcgaacgcgaggagcgcgagaaaatcgaagccctgcagcgggaaaagaatcgcatcaagtcc
ggcaaggacatgaccgaggccaagcggcgcatggaggagttggagatgaagaagatcgttgagcagcgcaagcgcgaaaa
ggacgaggagaaggcggcccgcgatcgggtaaaggctcaaattgaggcggacaaggcagcacgcaaggctagagaacaaa
aggaattgggcaacgcagagccagctccatccgtgagctccaccacagtttcgtcaccaccggccggtgtgaaatctccgccgc
gagactacaccgaaacccgcatccagggcgccagcgcaatcttggccgcagcggctccctactatcaaccgccggctgttccc
caggatgttcagccggatcgtcctatcggctatggagcattcggagttgtctgcggttcccacatcagcggctggcattgttctgcg
gggcattatgaagatggtaatgaaaatttcgagtgcctcaagacattttcgacttctgaccgcattggctgcgaatggagatgggcg
gcagcaactgttcttgccgcaacctgcattagcccgaacggccgttgcgggcattataaacgcgtacgtcgtcgcattaaaacaaa
cataacaactacgtga

***Drosophila* Gene Hit**	rescue sequence and BLASTX with EST: BIP1 (Y14998), BLASTX with genomic sequence matches BIP.
Human Homologue	BLASTX with BIP1: alanine:glyoxylate aminotransferase (X53414) ?
***Drosophila* EST**	GM04749 (AA695904), GM13608 (AA803601)

Annotated *Drosophila* genome genomic segment AE003556

Annotated *Drosophila* genome Complete gene candidate CG7574 - bip1 unknown function

CG13681 – unknown

Human homologue of Complete gene candidate none

Putative function no homologies to indicate functions, Drosophila Bip1 interacts with transcriptional activator Bric-a-brac which is required for ovariole formation

Confirmation by RNAi Both show reduction in G1 and G2/M iondicating fewer cycling cells

Example 52 (Category 4)

Line ID	763/4
Category	Meiotic defects in testis: segregation defects (overcondensation, fewer anaphases)
Reversion	R
Map Position	90F

Rescue ID 2F5E-1

Rescue Sequence
CGGCAATGTCTGCGCCCCCAATCTGAACTTGCCTCGCCCTCTCCGCCCCTGATC
TCATCTCCTCTTCAAACCCCTGCTCCCCTTTTCTGCACACATTAACGTCAGCCT
TTAAGTGTGCTTTCTCAGGTGCTGCCCCCTGCGCCCACCATCCCCCGCTCCATG
CTCTTTCCATCTTGCGCTCTCTGCGTTCTATCTACATTTTTTTCGAGGTCGCGCG
CTGCTTTTTCCGTTGATGTTCGTTCTCGTCAATGTCGCAATATGCGCAAAAGGC
AGACAAAAAAAAAAATGAGTGGAAAAAGTACATACATACCGGTGATTGATGGG
CGGTGGGTGGCGGTGGTGTTAGGNGTGGTTTG

Genomic hit, Accession No. AC006495

Associated ORF
Genscan ORF1 predicted sequences >22:47:02|GENSCAN_predicted_peptide_3|283_aa
MTERENNVYKAKLAEQAERYDEMVEAMKKVASMDVELTVEERNLLSVAYKNVI
GARRASWRIITSIEQKEENKGAEEKLEMIKTYRGQVEKELRDICSDILNVLEKHLIP
CATSGESKVFYYKMKGDYHRYLAEFATGSDRKDAAENSLIAYKAASDIAMNDLP
PTHPIRLGLALNFSVFYYEILNSPDRACRLAKAAFDDAIAELDTLSEESYKDSTLIM
QLLRDNLTLWTSDMQAEEIPIPKLPDRQSKTTLIFSPRSQVNPKILHKNNTIIGRVIC
SVFA

>22:47:02|GENSCAN_predicted_CDS_3|852_bp
atgactgagcgcgagaacaatgtgtacaaggcaaagctggccgaacaggccgagcgctacgacgaaatggtggaggccatga
agaaggtcgcctccatggacgtagagctgaccgtcgaggagcgaaatctgctgtcggtggcgtacaagaatgtgattggagcac
gccgtgcctcgtggcgcatcatcacctcgatcgaacagaaggaggagaacaaggggggccgaggagaaattggagatgatcaa
aacctaccgcggacaggtggagaaggagctgcgcgacatctgctcggatatactgaacgtgctcgagaagcatctcattccatg
cgccacatccggcgaaagcaaagtattctactataagatgaagggcgactaccatcgctacctggccgaattcgccaccggctcc
gaccgcaaggatgcggcagagaactcgctgattgcctacaaggcggccagcgatattgccatgaacgatctgccaccaacaca
ccccatccgtttgggcttggcattgaacttctcggtgttctactatgagattctcaactcgccggaccgcgcttgccgcttggcgaaa
gccgctttcgatgatgccattgccgagttggatacactgagcgaagagagctacaaagactcgacactcatcatgcagctgctgc
gcgacaacctcacattatggacgtccgatatgcaggcagaagagattccgattccaaaactccccgacagacagtccaaaacca
cattgatttttagcccccgaagtcaagtaaacccaaagattctccacaagaacaacaccatcatcggcagagttatctgtagcgtgtt
tgcgtga

***Drosophila* Gene Hit**	rescue sequence: 14-3-3 epsilon isoform gene (U84898) TBLASTN with ORF1: 14-3-3 .
Human Homologue	TBLASTN with ORF1 and BLASTX with 14-3-3: epsilon isoform 14-3-3 protein (U43430.1)

Annotated *Drosophila* genome genomic segment	AE003721
Annotated *Drosophila* genome Complete gene candidate	CG8045 complex gene appears to encode 3 things : Transcript: CT24102 unknown Transcript CT24072: transcription factor RNA polymerase II transcription factor , Transcript: CT24092: diacylglycerol-activated/phosholipid dependent protein kinase C inhibitor /14-3-3 protein epsilon (suppresspr of ras)
Human homologue of Complete gene candidate	CT24092: e-119 NP_006752.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide; 14-3-3 epsilon [Homo sapiens

Putative function transcription factor, or 14-3-3 proteins which associate with cdc25 phosphatases

Confirmation by RNAi CT24102: wild type profile only, CT24072: Loss of G1 peak CT24092: Increase of G1 peak

Example 53 (Category 4)

Line ID	951/8
Category	Mitotic defects in brain: (some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle)
Reversion	NR
Map Position	73D

Rescue ID 2E8S

Rescue Sequence

GTATAAACAAGATCCCGAGACACCGGTCAGTTGGTGCTACACGCTCTTGGAGA
GCGCTGTGTTTGTTCCGTTCAGCGATTAGCGATAGTTTTGTTCGAGCCGGTTGT
GTTAACTTGGCTAGCTTCGGGTTTATTGTGACACTTTCCCCAAATCGATCGTTT
GCGAAGCGTGCATAGCGGAACATACATACATAGATAACCAGCGTGTCTGGGT
GTTCATGAAAAAGAGTGCGTGATATGGGATTCGATATGGCAACACGCTTTATG
GATATACTAAAGCTGACCTTTAAGTGAGTTTTCCCAGTCAGTGTCCGCTTCTTG
CTCTTGCGGAGCGTTAAACGGTTTTCTGTGTTTTGAGGTCTCGCGTCTTGGTTT
TGCAACAGCTTCTGCCCAGCATGCACACATACGTGTGCACTGGGAAAATAGTG
TTGCAGAAGTGCTTGATTTATAAATATTACAAAAAATGTGATGAAACACTTTT
TATTTTCTTCAAAAAATCAAGAATAAATTAACACTATCCTGCTCTTAAAACAT
GGAGATTAATTCAATTTTAATTAAAAAATAATTTTTTTACAATTTATGATTTA
TGAATTTATGCACTCCTTGAAACTATTAAAGACTCAACAGTGA

Genomic hit, Accession No. CSC:AC015272

Associated ORF

Genscan ORF1 predicted sequences

>23:03:05|GENSCAN_predicted_peptide_1|602_aaMGFDMATRFMDILKLTFKPFKTN
YTEEKYFNDKLRSSKNIERRYILDVGFRGPTAVTYNPIWVISFKYEQRKLSTAIYSV
IKTKSGPVRGVKRNTIWGGSYFSFEKIPFAKPPVGDLRFKAPEAVEPWDQELDCTS
PADKPLQTHMFFRKYAGSEDCLYLNVYVKDLQPDKLRPVMVWIYGGGYQVGEA
SRGLDVVIVTVAYRLGALGFLSLDDPQLNVPGNAGLKDQIMALRWVQQNIEAFG
GDSNNITLFGESAGGASTHFLALSPQTEGLIHKAIVMSGSVLCPWTQPPRNNWAY
RLAQKLGYTGDNKDKAIFEFLRSMSGGEIVKATATVLSNDEKHHRILFAFGPVVE
PYTTEHTVVAKQPHELMQNSWSHRIPMMFGGTSFEGLLFYPEVSRRPATLDEVGN
CKNLLPSDLGLNLDPKLRENYGLQLKKAYFGDEPCNQANMMKFLELCSYREFW
HPIYRAALNRVRQSSAPTYLYRFDHDSKLCNAIRIVLCGHQMRGVCHGDDLCYIF
HSMLSHQSAPDSPEHKVITGMVDVWTSFAAHGDPNCESIKSLKFAPIENVTNFKC
LNIGDQFEVMALPELQKIEPVWNSFYAPNKL

>23:03:05|GENSCAN_predicted_CDS_1|1809_bp
atgggattcgatatggcaacacgctttatggatatactaaagctgacctttaagccatttaaaacgaactacactgaagaaaagtattt
caatgacaaactcagatcttcgaaaaatattgaaaggcgttatatcttggatgttggctttcgcggacccacagcagtcacgtacaat
ccaatctgggtaataagcttcaagtacgagcagcgcaaattgtcaacagcaatatattccgtcataaagacgaaatcaggtcctgtg
cggggagtgaagagaaacacaatctggggaggaagctacttcagtttcgagaagatacccttcgcaaagcctccggtgggagat

ctgcgcttcaaggccccggaagcagtggagccatgggatcaggaattggattgcacttcgccggcagacaagccccttcagaca
cacatgtttttcagaaaatacgcgggctcagaggactgcctctacttaaatgtgtatgtcaaagatctgcagccggataaactgcgtc
ccgtgatggtttggatctacggaggaggctatcaagttggcgaagcttctcgaggattggatgtggtcatagtcaccgttgcttatcg
actgggtgccttgggcttcctcagcctggatgatccccaactaaacgttcccggaaatgcaggtctcaaggatcaaatcatggccc
tgcgatgggtgcaacaaaacatcgaagcattcggcggtgattccaacaatattacactctttggcgaaagtgccggcggagcctc
gacccacttccttgcactaagtccccaaactgaaggtcttatccacaaagctatcgttatgtcgggcagtgttttgtgcccctggacg
caaccaccgagaaataattgggcttataggctggcccaaaaattgggatacaccggtgacaataaggacaaggcgatctttgagt
ttctgcgatcaatgagtggcggggagattgtcaaggccaccgcaacagttctcagcaacgatgaaaagcatcatcggatcctttc
gccttcggacctgtcgtagaaccatatactaccgagcacactgtggtcgctaaacaaccgcatgaactgatgcagaatagctgga
gtcacaggatacccatgatgtttggaggcacgagcttcgagggattgctattctatccagaggtttcaaggcggccagcaaccctc
gatgaggtgggtaactgcaagaatctgctaccgagcgatctcggtcttaacctagatcccaaactgcgtgagaactacggcttgca
actgaagaaggcgtatttcggcgacgaaccctgtaaccaggcaaacatgatgaagtttctcgagctatgctcatatcgagagttctg
gcaccctatatacagggcagctttgaaccgtgtccggcaatccagcgcacccacgtatctgtatcgattcgatcacgattccaaact
gtgcaacgccattaggattgtactttgcggccatcagatgcgaggtgtttgtcatggtgacgatctgtgctatattttccacagcatgtt
gtcgcatcaatccgctcccgattctccggaacacaaggttataaccggaatggtcgacgtttggacgagtttcgcagcccacgga
gatcccaactgcgaaagtataaaatcactcaagtttgcacccatcgaaaacgtaaccaactttaagtgtctcaatattggggatcagt
ttgaagtcatggcgcttccagaattgcagaaaatcgaacctgtgtggaatagtttctacgccccaaacaaactgtag

***Drosophila* Gene Hit** TBLASTN with ORF1: alpha esterase (aE10) gene (U51054)
Human Homologue TBLASTN with ORF1 and BLASTX with U51054: bile salt-dependent lipase (S79774)

Annotated *Drosophila* genome genomic segment AE003671
Annotated *Drosophila* genome Complete gene candidate CG1131 - alpha esterase 10

Human homologue of Complete gene candidate 4e-48 4557239 ref|NP_000656.1|pACHE| acetylcholinesterase (YT blood group) precursor >gi|113037|s

Putative function alpha esterase

Confirmation by RNAi Only wild type profiles observed

CATEGORY 5: SMALL IMAGINAL DISCS (BLOCK TO PROLIFERATION)

Example 54 (Category 5)

Line ID	113/20
Category	2nd chromosome, small imaginal discs
Reversion	R
Map Position	50D/E

Rescue ID EcoR1
Rescue Sequence 1
CTGAGGCNCTTTGCCAATATGTGTATATTGGGCGGGGNACATGCGTNAATCGG
TTAAAGCCGCTACTTACATTCTGTTCTTTGCATCTCCCCCATCCACAGCTATAA
AGCAAGATGAGCTACGCCGCTGATGTGCTGAACTCGGCCCATTTGGGAGCTCC
ATGGTGGTGGCGACGCCGAGTTGCGTCGTCCATTCGATCCCACGGNCCATGAT
TTGGATGCATCCTTCCGCCTTACACGCTTCGCANATCTAAAGGGGCGCGGCTG
CAAAGTGCCCGCAAGGAAGTNGCTCCCCCACCT

Rescue ID BamH1
Rescue Sequence 2
CCACCTGGTACCACAGCGCTCANACGTGTATGTACACGGATTTTCTGCCGCGT
GTGTGTAGCGCGGCCCGTGATTGGCTGCAGTCGCGATGGCGGCTAAAACGGG
CGAAGTCAGTATTTCTCCCTGTCGACGANGCGAGCAACGTGAACAATGCCCAC
TCATTTCAATTGCAAAATGCCAAAAAGTGCGCGCTTTGAATTGGCCATTTGGT
TCGTTGCGTTCGTTTGTCTTTTGGTACTTACGTTTGCTTGTGCGATTGTACAAA
GATAATTGTAGAGTAACGTTAGCAAATTATATTTATTTTGCGCCTGGTTTTTGC
TTTTCCAACGANCGAGATGTCACAACAGGGTTGTATTANCGTGTGCGGCTGAT
TCGATATTTGGGATGCCGATTGTCTGAAGCGANGGTTCAACGGGGCTGCCAAC
TCCCCCGAAAATCTATCNATGGTATTGTGCGCCAAGGGTAAAATAAATAAAAA
TATGTTAAAACCGCGGAATAAATGGGGGAACCGAAGTGGAAACTGTGGTTCA
CAGTGCTCTGACTTTCGGGAGCAGTTAATATAGTTGGCATTAATTCAATTAGA
GCTCCAAAGTGCTGGTCACAAAGAACGCACAAGAACGGGCCATGAAAAACCT
GTTGCGCCAGCAGAACGAAAAGTAAAAATTAGAAGAAACCAT

Genomic hit, Accession No.	CSC:AC017131
***Drosophila* Gene Hit**	rescue sequence: selenophosphate synthetase (ptufl) (U91994)
Human Homologue	BLASTX with U91994: SELENIDE,WATER DIKINASE 1 (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) (P49903)
***Drosophila* EST**	LD46437 (AI514756 similar by BLASTN to U91994 selenophosphate synthetase (ptufl) gene)

Annotated *Drosophila* genome genomic segment AE003815

Annotated *Drosophila* genome Complete gene candidate	CG8553 *selD* selenophosphate synthetase
Human homologue of Complete gene candidate	1711372 P49903 SELD_HUMAN SELENIDE,WATER DIKINASE (SELENOPHOSPHATE SYNTHETASE (1e-159)

Putative function selenophosphate synthetase

Confirmation by RNAi Only wild type profiles were observed

Example 55 (Category 5)

Line ID	121/1
Category	2nd chromosome, small imaginal discs
Reversion	NR
Map Position	60B

Rescue ID BamH1

Rescue Sequence

TCCTGTGCACTCATATTGATTTGCCTTGTCAAGTGGCTAAAGAAATATTAAATG
TTTGTTATTTCTGTTGCTAGCGCTCCGACAGTCTGGCAGCACTGCTCGCTGTCG
ATAGTTCAACTGAGTTGCTGTTTCATCGAACAGAGCTGCCAACTCTATTTTTGT
AGCTGGCCAGCCAGGATTGCCAGAGTAAGGCCCTCAAATCAGCTGTTTTGTGT
TTTGATTTTATTTTGAAAGTCCTAGTTTAAAATTATGCTTTCTCCGACAGATCA
GCACAAATAATACTAATAAAGCTCACAATGCTAAGGTTGTGCCTTCCAACTCG
AGCTGGATATGTGCGTAAGTAAGGACTTTACGTCTATAAAACTTGTTATGTAA
AGTAAATGTTTGCCTATTGCGCAATTTCTCCAACGAAAAACCCAGAAAACCNA
AACCCCCTTNAAANTTTGGAATATNCCCAATGAATGCAGCACCCGTGAAATCC
GTAATGCCTTTGTCCAGCTCTCCAAATTGGTAAGTAACTCCAAGATCCAAAGG
AGCCTCCTAAACCCTGCCCTTTCCACAGTACCACCCAGATGTTAAGAGCAATG
CTGCGTGTCCGGAGCGCACAGCCCGATTTGTTCAGATCTCCGAGGCGTACAAG
AACCTGATAAAGCCGGAACGGAAGGAAAAA

Genomic hit, Accession No. CSC:AC020499
***Drosophila* Gene Hit** rescue sequence: DnaJ60 gene for dnaJ-like protein (Y11900)

Annotated *Drosophila* genome genomic segment	AE003463
Annotated *Drosophila* genome Complete gene candidate	CG12240 – DnaJ60 CG13570 – spaghetti ser/thr phosphatase
Human homologue of Complete gene candidate	CG12240- 4827026 ref|NP_005138.1|pTID1| tumorous imaginal discs (Drosophila) homolog >gi|3372677 (AF061749) 7e-08 CG1116- 2495728 HYPOTHETICAL PROTEIN KIAA0258(aa)

Putative function CG12240 : Chaperone involved in protein folding
CG13570 : serine/threonine phosphatase

Confirmation by RNAi	CG12240: Marked reduction in G1 and G2/M peaks indicating fewer cycling cells CG13570: Marked increase in G1 peak

Example 56 (Category 5)

Line ID 127/2
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 57F

Rescue ID EcoR1
Rescue Sequence 1
GCCGGTGGGCCCACACTTGTNCGCCCGCGCATCGGCTGTCTGTGGGAGTGCGA
NCGAGTCAGATAGTAGATCCGATGCGCTCTCCAGATACTTTTTGAACACTGAA
GAAAACGCGCAGTTGTGGGTGAATTCAGCATCATCAGATTGAATCACACACA
ATCCTAGTCGCCTCACGCGAAGAGAACTATGTCATGATCAGATATCGGTGTAT
GCATTCTATATTATGTACTTCGAAATATGTAATTTATTAAGTTTTCGCTATACT
TTTCATTCAAATTGGCAAAAACCAATTCAAAGGTTTTCAATATTTTCGAAAAG
CATTTTAGGCTTTCTATGTAACGTATGTTTTTCAAACAAAATATTAGTTTTTGA
AACTTTATTATCGGATAAACAAATGTAAGCCAAATNACAACGTTNTATGATAC
TCCCAAAGATCCGCNCTNTTAAAGTGGCCTAAAAATAGCTGACGCATTAANCC
ATAGGCGCTTCGCTTCTCAAGATAAAACCTGGCGTGCTCAACTCAAGAAACAA
ATATGTGGTTATATACATATATACATATATGGGGCATATAACCGATGTGTGAC
GTGACATTGGCTCGTTCTATTCACATACTTAAACACTAAATGCAAACCTATCA
AAAACCNACTACACTAAGCGAAAAACGGCAGANATAGTTAAGGAAAGTGGTC
CA

Rescue ID BamH1
Rescue Sequence 2
CTTCTTTTCTCAAAAAACGTCGCTCGNGTCCCNCAATCGTTTTACAAACTTCGC
TCGGAACGGACGTGTGCGCGCTCTGAAAGGAAAAAGTGAAAAAGTGTGTGAC
AAAGTGCAAATAAGCCACAACGCGCATGTGAGAAATCAAATTTAATTGAGAA
GCATCAAAAATTGTATACATATCGAGCGTATCCACATCGCTGTATGTGTGAGT
GTGCCAGTGCTAGTGTGGTTTTCCCTTTTCGCCGTGGAAAATATGAAAACTGA
ATGAAAAACTGAATCGCAGTCAGCCAGAGCCGAATTGGAAAAGAGTAACTCG
CATTGGGGACACGAAGAGGTGTCTCGAAAAAGGTAAAATCTTTTACACAGAA
ACGACGCCAGAAAGCGATTAGCGATTTNTGACTATGTGTGAGTGTGTAATTTC
GGTCTACGGCTGTGTGTCTGCATTTTATTTAACNTTTTGTTTCCCNGTTNGNTC
CACNGTAAAAATAGCTAAAAAAAAAGGGCAAGTACTCTTGGCGCGCTCTCCC
TCTCTCTTTGTTGGTCGTGACTGCGACGTCACCGTTCACGTAGAATCGTTTTCA
AGTGGCGTTTCTTTCTTTCTTTTTAATGTGCTGCTTCTTGCTTCTGCCTCTTCTTC
TTGCCTTTGGCTATCTGCTTTGTTTTGAAATACGTCCATGTTATTCCAGTGTCTG
TGCCAAATGTGTGCGANATGATCTCTACTT

Genomic hit, Accession No. AC009732

Associated ORF
Genscan ORF1 predicted sequence
>/tmp/aaaaafrla|GENSCAN_predicted_peptide_2|456_aa

MQTKGPITDADCIRGMACRALAGLARSDRVRQIVSKLPLFASGQLQTLMRDPILQ
EKRAEHVIFQKYALELLERVSGKTKPLNNPLDPSLSNMHKANVIAQTRIQYNKQQ
LYQLIFEHLESNGLSQTAQMLQREVGLPLQTPTTRSFHQSPFDYKSLPSGSSSLSRN
RLRSRMQDVNAAIMGNGDLNRSFGEDSSPAGAGGSNAGDGVSIPNFSSLNTTQTP
IKIRRTDRSSVSRSIQKQAMEPGGMSVGLAEDGQLHPKRITLNTIVTEYLTNQHSL
CNNPVTTCPQFDLYEPHKCPDPKPSRLLSSNYNLTSRHARTQAGFNTSRFDRRYV
HTHFSPWRSIRSADYEDLEFTCCDLAGKYIIVGTQQGDGRVFNMNDGVEQFFSNC
HNFSVDAIKANRAGDLVITSSFWRTPTSILWSIADDEFKLKLRLPDVTYCEFSQTV
QDRLLGTQNEVY

>/tmp/aaaaafrla|GENSCAN_predicted_CDS_2|1371_bp
atgcagaccaaaggacccattacggatgcggactgtatacgtggaatggcctgtagggccttggcgggacttgctcgctccgatc
gggtcaggcagatcgtcagcaagcttccactctttgccagcggacaactccagacgctgatgcgggatcccatactccaggaga
agcgcgcggaacatgtaatcttccaaaagtacgcattggagttgctagaacgagtgtcgggtaagacgaaaccgctaaataatcc
tttggatccatcgctgtccaacatgcacaaggccaatgtaatcgcccagacacgcatccagtataacaagcagcagctgtatcagc
ttatcttcgagcacctggaaagcaacggtctctcccagacagcccaaatgctgcaacgggaggtgggtcttccgctacagactcc
cactacgcgcagttttcatcaatcacctttcgactacaaaagtcttcccagtggtagtagctcgctgtctagaaatcgtctgcgaagc
cgcatgcaagatgtgaacgcagcgataatgggcaatggagacttaaacagaagttttggtgaggactcctcgccggcaggagcc
ggtggtagcaatgcgggagatggagtcagcataccaaattttagctcccttaacacaacgcagacgcccataaaaataaggagg
acggatagaagttcagttagccgctctatccagaagcaggcaatggagcctggtggcatgtcagttggtcttgccgaagatggtca
actgcatcccaagaggatcaccctaaataccatcgtaacggaatacctcaccaaccagcactcgctgtgcaataatccggtgaca
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ctagtcggcatgctcgaacccaagccggatttaataccagtcgctttgaccgtcgctatgtgcacacgcacttttcaccatggcgta
gcattcgatcggcggactacgaggacctagagttcacctgttgcgatttggcgggtaaatacatcattgtgggcacgcagcaggg
cgacggacgagtgttcaacatgaacgatggcgtggagcagttcttctccaactgtcacaactttagcgttgatgctattaaggctaat
agagccggagacttggtcatcacatctagcttctggcgcacacccaccagcattctatggtctattgcggacgatgagttcaagcta
aagttgcgacttcccgatgtcacgtactgtgagttcagtcaaacggtgcaggatcgtttgttgggcacccagaatgaggtatactaa

corresponds to CG10082

***Drosophila* EST** several including SD04293 (AI532704)

Annotated *Drosophila* genome genomic segment AE003454

Annotated *Drosophila* genome Complete gene candidate CG10082 – novel protein with homology to enhancer Pi uptake

Human homologue of Complete gene candidate 1665793 dbj|BAA13393| (D87452) Similar to S.cerevisiae YD9335.03c protein (S54640) [Homo sapiens] (2e-43)

Putative function Putative phosphatase or enhancer of Pi uptake protein

Confirmation by RNAi Reduced G1 and G2/M peaks indicating fewer cycling cells

Example 57 (Category 5)

Line ID 131/8
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 60A

Rescue ID BamH1
Rescue Sequence 1
CACGATTGCNGGCCCATCGAAGTGTGGGTCTATCGATACTCGTGGGTAAATAA
ACAAGTTCTGAACTGCGATTTCGGGGGTTTGAGGGGTCAATTGTCCCCTGTGT
TGGAATGTGTTCCTAAATCTACACAAACACTCCCTAAGCTTATCCTAAACTTAT
AAATATTGGTTGCTATTTAAACCCCATTTCACGGTTATCCAGCACGCCCCTGA
ACTGTGACCCACATCCCCGATTTTAGTGACTAGTTTTATACTTATCGTGGTTGG
CATTTGGTACACTACACTTTCTTATTCACCTAGATCGCCGACTCCGCGCACGGT
CGCGCTCCCGTTCCCGCTCCCGATCTCGGCTGCGACTGCGGTCGCGATCCCGTT
CCCGGTCGCGGCGACCGGCGCCTCCANATCCGGATCCCTAANCGGCANCNGT
CNTGGTGGCAATCNNGGAATGTTCCGGGGNNCCNCTACCNCAGTGNAATCAC
TGGTACGTCCCACCGCNAAACTCCGCCCANTGCGGTTGCCGGAACGGGTGGC
ANTGCCAATGGGTCGCTGCAGAAGGTACCATCACAGCAATCGCTCACGGANC
CCGAAGACTGCCTCTGCCGCCCGGCTGGGCCACTCATACACGCTACACGGTCG
GAAATACTACATTGATCACAATGCGCATACCACGCACTGGAATCATCCGTTGG
GAACGC

Rescue ID EcoR1
Rescue Sequence 2
AATTGATTTCCGGACATATAAACAGAATCCAGAACTCATCCGGCAGCAGGCTC
AGTCAGGCCAGTAAATCCGAAAAGAGAGTAACCAGCAGGAAAAGAGAATCC
ACGTAAATACAGAGAAAATGGCTCTACGCGTCCAATTCGAGAACAACGACGA
CATCGGCGTATTCACTAAACTAACCAACACATACTGCCTGGTGGCCATCGGTG
GATCCGAGACCTTCTACAGCGCCTTCGAGGCGGAGCTGGGCGACACCATCCCG
GTGGTGCATGCGAATGTGGGCGGCTGCCGGATCATCGGCCGCCTCACCGTGGG
CAACCGCAACGGCCTGCTGGTGCCCAACTCCACCACCGACGAAGAGCTGCAA
CACCTGCGTTACANCCTGCCANAACCCCGGAAANATTTATCGTGTGGAAGAAC
GCCTGTCCGCGCTGGGCAACGTTATCGCCTGCAATGATTATGTGGCCCTGGTG
CACCCGGATCTGGACAAGGAGACCGAGGAGATCATCGCGGACGTGCTCAAAG
TANANGTCTTCCGCCAGACCATTGCCGACAACTCACTGGTGGGCTCTTACGCC
GTGCTGAGCAACCAGGGGGGCATGGTGCATCCCAAGACNAGCATTCAGGAAC
AGGACAACTGTCGTCCCTGCTGCAGGTTCC

Genomic hit, Accession No. CSC:AC020517

Associated ORF
Genscan ORF1 predicted sequences >22:13:05|GENSCAN_predicted_peptide_4|357_aa
MALRVQFENNDDIGVFTKLTNTYCLVAIGGSETFYSAFEAELGDTIPVVHANVGG
CRIIGRLTVGNRNGLLVPNSTTDEELQHLRNSLPDAVKIYRVEERLSALGNVIACN

DYVALVHPDLDKETEEIIADVLKVEVFRQTIADNSLVGSYAVLSNQGGMVHPKTS IQDQDELSSLLQVPLVAGTVNRGSEVLAAGMVVNDWLSFVGMNTTATEISVIESV FKLNQAQPATVTTKLRAALIEDISRSRVAGGGGGGGGGGSSGGNSSSGPSTSRRTT RNNAAATAADRPKINEADLEGKSPEEVEMLKTMGFCTFDTTKNRKVEGNDVGEV HVILKRKYRQYMNRKGGFNRPLDFVA

>22:13:05|GENSCAN_predicted_CDS_4|1074_bp
atggctctacgcgtccaattcgagaacaacgacgacatcggcgtcttcactaaactaaccaacacatactgcctggtggccatcgg tggatccgagaccttctacagcgccttcgaggcggagctgggcgacaccatcccggtggtgcatgcgaatgtgggcggctgcc ggatcatcggccgcctcaccgtgggcaaccgcaacggcctgctggtgcccaactccaccaccgacgaggagctgcaacacct gcgtaacagcctgccagacgccgtgaagatttatcgtgtggaggagcgcctgtccgcgctgggcaacgttatcgcctgcaatgat tatgtggccctggtgcacccggatctggacaaggagaccgaggagatcatcgcggacgtgctcaaagtagaggtcttccgccag accattgccgacaactcactggtgggctcttacgccgtgctgagcaaccagggcggcatggtgcatcccaagacgagcattcag gaccaggacgaactgtcgtccctgctgcaggttcccctcgtggccggaacagtgaaccggggcagcgaagtactcgccgccg gcatggtcgtcaacgactggctctccttcgtgggcatgaacaccacggccacagagatctccgtgatcgagagcgtcttcaagctt aaccaggcacagcccgccacagtgacgaccaagctgcgtgcggccctcatcgaggacatatcgcggtcgagggtcgccgga ggaggaggaggaggaggcggcggcggaagcagcggcggcaacagcagctccggaccatcgacgtcgcgaaggacgacg aggaacaatgcggcggccacagctgccgaccggcccaagatcaacgaggcggacctggagggtaaatcgccggaagaggt cgagatgctgaagacaatgggattctgcacgttcgacaccaccaagaacaggaaggtcgagggcaacgatgtcggagaagtgc atgtaatcctcaagcgaaagtaccgccagtacatgaatcgcaagggtggcttcaaccggccgctcgatttcgtggcatag

***Drosophila* Gene Hit** rescue sequence and TBLASTN with ORF1: b(2)gcn (EUKARYOTIC TRANSLATION INITIATION FACTOR 6)((X97641)

Human Homologue BLASTX with X97641: integrin beta 4 binding protein (HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 6) (NP_002203.1)

***Drosophila* EST** GH08760 (AI109537 similar by BLASTN to X97641 "D.melanogaster b(2)gcn gene.")

Annotated *Drosophila* genome genomic segment AE003462

Annotated *Drosophila* genome Complete gene candidate CG17611 – bcgn benign gonadal neoplasia homology to Eif6 translation factor

Human homologue of Complete gene candidate 6016331 EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6)(aa) and 4504771 |ref|NP_002203.1|pITGB4BP| integrin beta 4 binding protein(aa)

Putative function eukaryotic translation initiation factor 6 (eif-6)(aa)

Confirmation by RNAi Slightly reduced G1 and increased G2/M indicating block in G2/M

Example 58 (Category 5)

Line ID	135/25
Category	2nd chromosome, small imaginal discs
Reversion	NR
Map Position	24A

Rescue ID EcoR1

Rescue Sequence

ATAACATGGGCNCTGGTTTTTAAGTNAAGCTCTANTNATTGGCCCCCATTCTTA
NNCTCTCTCGCTCTCTTCTCGCTCTTTCGCCTGCTCTCTCGCCTGATTATTCTGC
TTGGTCGGCTGATGGTTTTNGTTTTNATCTGGTGTATTTTCTGCGTAGTTTATG
ACAAACCGGCTGGTTCTTGTTGTTATTGCCGTATTCTAATATATTCCCCTATTG
TTCTTATTTTTGTTGCAGCCTGCACACCTCGGAGGTTCTAGATGATAAGGGGTG
TAGCGATGGTGGGGGGCTGTCTTGANGGGCTTCTCGCCTTGAGCTCTTGTTTAT
CTTTGGTCATTTGTTATTGTTTAATGCACGGCAATATTATTGGTAAACAAGTTA
GCCAACAGCACTAAACGCCAATCGCATTCTTTTCTAAAAACCAAGTCTATTGT
CGATCTTGCTAGGGAAATGATGATGACTCAGGTGCAATTGGGATCTTATCTAT
GGCTGTCTGGGAATCAAGAAGTGTTCCCGCAGAATTCGTGAANTACTGCCGCT
CTCTCCATGGGGCCATTATTTGCACTCGTTTTNCGCGAAATACCATNAATTAGC
ATAAAGACACGTCGCCGGCAATCGTGACGTAGGCTATNAATGCCTTCTATGCA
TGTGCNAACTCGCGGAAGCATAGCAATTTGAAGGAACAATATTTCANTGCAG
GTTTTAATGGGCTAAAAAA

Genomic hit, Accession No. CSC:AC014199

Associated ORF

Genscan ORF1 predicted sequences >20:54:54|GENSCAN_predicted_peptide_3|117_aa
MSASPTARQAITQVMPMITRKVVISDPIQMPEVYSSTPGGTLYSTTPGGTKLIYER
AFMKNLRGSPLSQTPPSNVPSCLLRGTPRTPFRKCVPVPTELIKQTKSLKIEDQEQF
QLDL

>20:54:54|GENSCAN_predicted_CDS_3|354_bp
atgtccgcttcacccaccgcccgtcaagccatcacccaggttatgcccatgatcaccaggaaggttgtcatctcggatccgatcca
gatgcccgaggtgtactcctcgacgcccggcggaaccctctactccaccactcctggaggcaccaaacttatctacgagcgggc
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ctcccttccgcaagtgcgtgcccgtccccacggaactgatcaagcagaccaagtcgctgaagattgaggaccaggaacagttcc
aactggatctgtag

***Drosophila* Gene Hit**	TBLASTN with ORF1: BcDNA.HL08053 mRNA (AF132557)
Human Homologue	TBLASTN with ORF1 and BLASTX with AF132557: eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2) (L36056)

Annotated *Drosophila* genome genomic segment AE003579

Annotated *Drosophila* genome Complete gene candidate	CG8846 - phas1 translation initiation factor 4E binding protein 2
Human homologue of Complete gene candidate	CG8846 - 4758260 ref|NP_004087.1|pEIF4EBP2| eukaryotic translation initiation factor 4E binding protein 2 (4e-16)

Putative function EIF4E translation factor binding protein

Confirmation by RNAi Slight reduction in G1 and G2/M indicating fewer cycling cells

Example 59 (Category 5)

Line ID 141/12
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 21A/B

Rescue ID BamH1
Rescue Sequence
GGCTCTTTTCCAAANAGGCAGTTTCTTGNCCCATTTCTTGGATTGCTTTGTAGT
GAACTNAATCGTTTTGTTGGTTCCTCTGTCGTCCAGTCTTGTGAAAATTTCGTG
ATAATAATGCCTGGATAAATANTTAAGCATTTGGAAAACGGGGGAAAAAGGG
CTAAGTTGTGTGAAGGAAACAATTGAAGTGACCCTTTGTNTATAAACATTCCA
CGACGTGTTTCGAAAACAAACAAAGATATGCGGAAACAAAGTGTTAATAAAA
GAGCNAAAAATAGAGAGAGAGTGTCGCGATAAGCGGTTGAGCGAGATAGAG
AAAATTGTTGATTAAAATGTGTGTCNAAATAAAACATCAAGCCGCTTGAACGA
ACAGTCAGTTAGTTGCTTCTGATAATAACCATGGGAAGCGGCNCGTGTGCTTC
GCTCCTCGTTACTTATAAAATATTTAAACGTTTGCATTCTTCNTATTTCCGAAT
TTTTGCNCCCCTGAANCAACTTNGTTAAACTGCAAATAGCAATGCAAACAAAC
GAATAGAAACTGAAATCGACAACNACATGTGAAATTCACAAATCAAATCGCA
ATTGTCATCCCAAAGATATAGAACAAGCTATAGGGAAGATANAGAATGTAAG
TGCCAAACTAAAATAAACAAACAAGAATAACATTTCCACAGGTGTTTTGCATT
TCAAATGCATATTTCCGTGGCGGNTACAAATCTTTTCAAAACCG

Genomic hit, Accession No. CSC:AC017815

Associated ORF
Genscan ORF1 Predicted sequences >17:48:30|GENSCAN_predicted_peptide_2|554_aa
MSNKKMFNRTTSVSPGQLHYYHTDFYYSMPDLHKTRKMHGVKRVLVFCLMIVIL
PAILIIMPLHLRKTVFADVIYPMAESDIIEIRAGISSIFCSKHTLRMNSNFNAFQLRNK
PEIATNRKHIRLKKSMTLPDDTLEYWGFFLLKGAKVRVKFCSRYDGSRILIIHGHR
ELNLCGLTDHNKNKLGANYAKGHEQVQVFFEDNVEITEEKGNQDVLMEHENHG
GEDLTEDIPQPQVNIPVKQNNSIQPKLIRKKLKKGTIHHGEHDMHAITDLQGSHHT
EHILNHHDHSSNSPAHHHNSTAHHREHSSNITNEETSRNHIRNEDEDPDQNSSKTH
YSAESPPHRERLKRHNRVAHRNQKRQDLYDTLYKRSKRENVYDRKTIHGGNAIN
FTETDESNSVSSFETGLFQCFNGMILLQEFFRPKNECSNPHIMDTSPNKSSMVVHN
VIEDGYYYYIFYSDNDHVQNEIHAIFDIYKPTYQYSNMSESQSCLNTTNCTFNISFL
SDEIVVVEVPTRDGIEHEEDDITNLISTCHPRSEIYAIFPITVLVLILCCSFL

>17:48:30|GENSCAN_predicted_CDS_2|1665_bp
atgtccaacaaaaagatgttcaacaggactacgtcagtaagtcctggacagttgcattattatcacacggatttctattactcaatgcc
ggatttgcataaaacccgcaaaatgcacggcgtgaaaagggtgctggttttctgcctgatgattgtgatactgccggccattcttatc
attatgccgctgcatttgcgaaagacggtgtttgccgacgtcatctatcccatggcggagtccgatatcattgagattcgggcagga
atctcgtcgatcttttgctcgaaacacacactgcgtatgaactccaatttcaacgcttttcaactacgtaataagccggaaattgcgac
gaatcgcaagcacattaggctgaagaagtcgatgacattgccggatgatacgcttgaatactggggcttcttcttgctgaaaggtgc
caaggtgcgagtgaaattctgctcccgctacgatggatcccgcatcctgatcatccatggtcacagggagcttaatctttgcggtct

gaccgatcacaataagaataagttgggcgccaattatgccaaaggtcacgaacaggtgcaggtgttcttcgaagacaatgtggag atcacggaagagaagggcaaccaggatgtgctaatggagcacgagaaccacggcggagaggatttgactgaggatattccaca gccgcaggtgaacatacctgtcaagcaaaacaattctatacagcctaagttaattaggaaaaaactgaaaaagggcacaattcatc atggcgaacatgatatgcatgctataacagatttgcaaggatcacaccatacggaacacatattgaatcaccatgatcacagctcta attctccagcacatcatcacaatagtactgcccatcatcgggagcacagttcgaatatcacaaacgaagaaactagtcgtaatcaca tacgaaatgaagatgaagatccagatcagaattcaagtaagacccattatagtgcggaaagtccgcctcaccgggaacgtctcaa aagacacaatagggtagcccataggaatcagaagagacaggatctttacgatacgctttataaaagatcaaagagggagaatgtc tacgatagaaagacgatccatggaggaaatgctataaattttacggaaacggacgagtcgaattcggtgtccagctttgagacagg actatttcagtgtttcaatggaatgatcctgctgcaggagttcttcaggccaaaaaatgaatgctcaaatccgcacataatggacactt cgcccaacaagagttccatggtggtgcacaacgtcatcgaggatgggtactactattatatattctacagcgacaatgatcacgttc aaaacgagatccacgccatattcgatatttacaagccgacgtatcagtactcaaacatgagcgagtcacaaagctgtctgaatacc acaaattgcacattcaacatcagtttcctttcggatgagattgtggtggtggaggttccaacacgggatggtatcgagcacgagga ggacgatataaccaatctgatctccacctgtcatccgcgcagcgagatatacgccatctttcccattacggtgctggtgctgatccttt gctgctccttcctgtag

corresponds to CG9524

Annotated *Drosophila* genome genomic segment AE003623

Annotated *Drosophila* genome Complete gene candidate CG9524 - novel His-rich protein

Human homologue of Complete gene candidate none

Putative function No homologies which indicate function

Confirmation by RNAi Reduced G1 and G2/M peaks indicating fewer cycling cells

Example 60 (Category 5)

Line ID 146/2
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 26B

Rescue ID EcoR1
Rescue Sequence
TTTNATCCAAACTGAGANACTNTTGGCCCCAAAACTGAAAACTCGGACTCGGG
CGCGTAAGGGAGTCGGTCNTCGGGAGTCGGTCGTCTTTTGTTGATCTTGAGAC
TGAAATTCCAATTGTTGATTTATCTCTCGGCTGCTGCGCCGCGGCTGCGCTGCT
GCAGCGCAGTCCCACTCCGATTTGACCAGCGACCAAGTTTATAAAACTTTGAG
CCAAAATGCAGCGGCGCACAGTTGTTACCAAAACGTTGCACGCGTCGTGGCCC
TCATCAAAACAAAAAAAAAAATATAAGCGAAAATGAAAACGAAATTCGGTTA
ACGTCAACAGAAGCTGACAAAAGGCAGAAAAGACCGAAACAAGTTGCAGGG
CCAGAGTAAGCCAAGTTAAATGCGAAAGAGAAGCAAGAGNCAAGAAGAAAN
AATGGGCACTACATACATATATTATAGCCAGCTAATCTGTTGTGCAGTGCGTT
TTATCAGCCNNCGAAAAGAAAACGAAAACGAAAAGTCGGTCCAAGTTCGGAC
TCAAAATCCAAACAGAAGAGACTCCATNCCATCAGAGACACGCGGATCTCAT
CTCGGTAATGTCTCAATAAAAGTAATCTTAACTGCCGCCGGGAATGTTGGAAA
AAGTGAAAATTGAAGCGCTTAACGTGTTTCGAAATACGATACATGAGAAGTCC
CAAAAAAAAAAA

Genomic hit, Accession No. CSC:AC019865
***Drosophila* EST** GH19286 (AI388389)

Annotated *Drosophila* genome genomic segment AE003481
Annotated *Drosophila* genome Complete gene candidate CG11353 - novel with weak homology to sugar acetylase?
CG7525 - tie receptor protein tyrosine kinase.

Human homologue of Complete gene candidate CG7525- 4e-23 4557869 ref|NP_000450.1|pTEK| TEK tyrosine kinase, endothelial >gi|464868|sp|Q02763|TIE2_

Putative function Sugar acetylase and receptor tyrosine kinase

Confirmation by RNAi Both gave a reduction in G1 and increase in G2/M peaks indicating arrest in G2/M

Example 61 (Category 5)

Line ID 155/13
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 21B

Rescue ID BamH1
Rescue Sequence 1
GNTTTAGTCCNCTTTTGANAGGGNCTTGGNGNCTTAAANAANNAAAAAAGGG
GNCCCGGCNCCCAGCAAANAGNNTAAAACTTGAATGGTTTAATTCGAAAATC
TTTTAGAAATGTCGCCTAATACCTTATCGGTATAGAGTTCACCTCGTCTCCTAA
TCCATATTTTAAGATATCAATATCTATTAACAATTTTTATCGTATGATTAGAAA
TTCGCATTGTTTTATTATTTCGACCTTTGGGCTTTACATCGACAGCTACTCTCTA
TCCAGACAGGAGACTGGGAGAGAGAGCACGATGCTGTCTGAAAGCATGAATG
ATGGATGCTGTGCCTATGTGCGATATGCACGTTGCCTGAGCTAAAACGAAACG
AGATTATTAATCTATCCGCAAGATTCAGATGCTGATTCCACATGAGTGAGCGA
GTCCGTGAGTGGATATTGCTCTCTCCGAAATGCATGCATGAGTGAGCAGGGGG
GCTTCAATCGCNCTNTCGATNTGCGACAGNGACATNTTTTTATCTTCGACNAT
GCNCTCNCTCCCTCCCACAGAAATCTTGCGCTNGNTCTCCGANNTNGGGNTNG
ANGGCNCTCTTCTCTNTCCTTAAATTGGGANTTNNCTTTTTCNAANAAGGGN
NAGA

Rescue ID EcoR1
Rescue Sequence 2
AATCNTTTTNTCCATTNGGCGNCTTNCTCAAAACATATTCACATTTGGNCCCAA
CGGCGTANGACTTNATCTCACGATTGTTTGGTTTCCTACTCTCCCGCGCTCCCT
CTCTTCTGAGTCTCTTTCTGGCTGATTCGCATTCGATTTTAGCCGCTGCCATCG
CCGTTGTTTTGCCTACCTATGTGTGTGTGTGAGGAGTGTGTCTTGTATTTCAGT
CCGCAATGCGCTCCGCTCATTATTTGTTTGANCGCCGCGGTGTAAAGTTGTAA
AAAGTCCAAGTGCTCGTGGAAACTCGATGCAAGACGGGGAAAACGAAACGCG
ATAAATCGTGAGAAAAGAGAGTGCGCTAAAGGAAGAGGGAGTGATAATCAN
ACGAAATGGAATAATGTNTTTGCAGAGGCNACAACAACAATGCAAATAGTTG
TCATTGAGGCGCAATGAATGATAATTAGTGCTTANTTGAAATCATAATCNTGA
AGAAAGCGTAAAGCTCGATTNTGGCAATNTATTCTTGATTACCANTGAGTCTG
TGATATTGCCGTGTGTNCCGAAAATGGANGTTATNAAACCCATGGACTTCAGC
ACCTTCTCCGCGTTCTGCGAACATCTTAACAAATCTCCACAAAATTGCAGCAA
CAACTGCANCGACGGTACCGCCAACTATAANCAATGGAAAANGCATTATTTG
GAGGTAANAGCNAAAAATACCAATNTTTCCAATGCGAAATTGCNAGCNTGG

Genomic hit, Accession No. AC004274

Annotated *Drosophila* genome genomic segment AE003590
Annotated *Drosophila* genome Complete gene candidate CG13693 - novel

Human homologue of Complete gene candidate 6e-05 4507659 translocated

	promoter region (to activated MET oncogene) >gi|1730009|sp|P12270|TPR_ HUMAN POOR MATCH
Putative function	No homologies to indicate function
Confirmation by RNAi	Only wild type profiles observed

Example 62 (Category 5)

Line ID 162/24
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 55C

Rescue ID EcoR1
Rescue Sequence 1
TTTTNTTTCANGGNTCTTTGCNCATAAAANACACGNGCCCTCNTGTCCATTCAC
ATTTTACTTGGAGTCGGTAACGTTGAGTTCCGCGTCCGTGCGTTCTGCCTTCCA
ATACAAAGTCTGGTGTGAATCTACCAAGCATTCCAGTGNGAAAATCAACTCAC
ATTGCTCGGTGATCCNTGCGGCGGTATNATCGCACCCGGAATTGCATAAGTTG
CGGNGAGCGGAAAGAGAGTGCACGGATTTNCNGTTATCNAAGGGCCGGCANC
NGTGGGGCGGCGACGGNAGAGCACGCAGAANAANAATANANTGNNGTGGCG
AATTNAAAAATANNATNAAAGAAAATTCGGGCCGCTAATTTTTCTTCAAATTT
GTGTGCGGTCGGCGAAAAACAACGTGTTTTTCNATGGTTGATAATACACACGG
ACGGNNCACTCGCGCTCACCCACATAGTCACNAAAGTCGGCGACGTCGACGA
CCCNCACNCTCACATANGGACNTTTAATCCCGTNCATNCGTGTAGCGTNCNTA
TTTAACCNTNTCTGTCCATCGGAACGCNCGCNTTCTCGCCTTCNTTCTNCTTTA
CTTTAATTTCCTATTTNNAAGGGGNAGNCCNATCTTTTTNCCTNTCNNTGCCNT
TTAANNTCATCCACANCCTCNCTTTNTCNTTCCTCCNCCTTNTNTTCTTTTCNTC
TTNCTTNTGNCCTTGCCTCGTTCTTTCTCTTCNTCTCCTTNCCCTTCTCCTCCTTT
TTTCTCCTTCCCCCC

Rescue ID BamH1
Rescue Sequence 2
AAGNCNCCTTGGCCGNNTTNAACGGNAANTAANCCGGGNCCNCGGGNCNCGA
TAATCAGGTCNANCCTTGTGCCTACCACCACCAAATTGAAAAAGAGCNAAGA
TTCTCTAAGGCAAAAAACTCCCCAATCTGTGGAATTTCCGGAAGCGAGAGCAC
ATTCAAAGCTACCAGTTATCAGCGAGCAGCATGTCTAAGCTCAGGAACCTGTT
GCCCACAATCTTTGGCGGGAAGGAGGCACAGAATCCGACACCCGTCGAGGGA
CGCCTGGAATAGGACGCAGCTCCCGTGGACGACAACGAACCNGATTACTACT
ACTGCGGAGCCATGGCGCTGCCCTCCACCGCTGGCACGCCCACAGCCTCCTCG
GATCTGACCGAATCCGTGCTGCGCGAGCTCAGCGACCCAAACTACAATTCAAT
GGATGTGGTGCTTTCNNCCTNTTTTCCGGGCACTCTCAGTAACGTCCAGACAA
ACAACACCATGAACGTTCACNGCGCCCAGCAACAGGTGGTCATGAACTTCTCG
AATGCCAATAATCTGCACTTCGGCTCCGTCTTCAACTTCAACCAAAACTTGAG
CGCCTGCNGCTCNCGAANGGGTTTCACCNGTTCGCANAAGAATCGGTCGCCTC
TCCANACNGT

Genomic hit, Accession No. CSC:AC012981

Associated ORF
Genscan ORFs: ORF2 predicted sequences
>18:26:17|GENSCAN_predicted_peptide_7|1320_aa

MEETNNATTIEQQPIALINGQEQVANEQQPSSPTSVATPTSTTSGGTGNATPAFSY
DDLFPALPANTSAQSQSGASGSTLARVTSSQKTHIVHVPCKERKSTESEKFGEGES
KRICQQITKETGAQIEIASRQVTVPREHFRVILGKGGQRLREIERVTATRINIPSQSD
ESEFITIAGTKEGIAQAEQEIRQLSAEQYKKSSDRITVPKVYHPFIVGPYSENLNKLQ
EETGARINVPPQQVQKDEIVISGEKDAVAAAKAKVEAIYKDMEKKCSTVSVEVAK
PKHRYVIGPKGSTIAEILQLTGVSVEMPPNDSPSETITLRGPQVALGNALTVVYQK
SNSVKSVEINAAHWIHKYVFGRKGANMKQLEEDCPNVNVNCLEDKIKLEGDPEN
VDRAVAYLSEIIKNYEENFTFEVMTVNPSYYKHIIGKAGANVNRLKDELKVNINIE
EREGQNNIRIEGPKEGVRQAQLELQEKIDKLENEKSKDVIIDRRLHRSIIGAKGEKI
REVKDRYRQVTITIPTPQENTDIVKLRGPKEDVDKCHKDLLKLVKEIQESSHIIEVPI
FKQFHKFVIGKGGANIKKIRDETQTKIDLPAEGDTNEVIVITGKKENVLEAKERIQK
IQNELSDIVTEEVQIPPKYYNSIIGTGGKLISSIMEECGGVSIKFPNSDSKSDKVTIRG
PKDDVEKAKVQLLELANERQLASFTAEVRAKQQHHKFLIGKNGASIRKIRDATGA
RIIFPSNEDTDKEVITIIGKEESVKKAREQLEAIIKECDEVTEGEVSVDPKHHKHFVA
KRGFILHRISEECGGVMISFPRVGINSDKVTIKGAKDCIEAARQRIEEIVADLEAQTT
IEVVIPQRHHRTIMGARGFKVQQVTFEFDVQIKFPDRDATEPVEGLTNGGSGENG
GENEGQEGEQEVEKEAEQEPVRQCDVIRITGRIEKCEAAKQALLDLIPIEEELSVPF
DLHRTIIGPRGANVRQFMSKHDVHVELPPSELKSDVIKVCGTPARVAEAREALVK
MIEDYEADRADRELRSFVLQVDVDTEFHSKLIGRHGAVINKLRADHDVIISLPKRD
EPNDRIISITGYQANAEAARDAILEIVGDPETLHREVIEIDKRIHPHLIGQRRRTIRKII
EDNKVNIKFSADDDNPNSIFISGKIEDVENVKELLFGMAEDYERDYLDNVAIAPPTI
GAFLTGFWIRCRRCQRERIRHQRRTVGEAKAGQKPDCAQHSVAGGLPALRCWRG
SGGLHAYHLRVGPQKLSASGRVSRSPAVAAILQVGVRRGSELEMDQELEQKLELE
LELDYRAMSGRAAAVVRTSL

>18:26:17|GENSCAN_predicted_CDS_7|3963_bp
atggaggaaactaacaacgcaactaccatcgagcagcagcccatcgctctcattaatggccaagagcaggtggccaacgagca
gcaaccatcctcgccaacttcagtggccacgcccactagtaccactagcggcggaactggcaatgccacacccgcctttagctac
gacgacctgtttccggccctgccggccaacacttcggctcaatcgcaatccggagcttccggttcgactctagctcgtgtgacgag
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cgtatttgccagcagatcaccaaggagaccggagcccagatcgagattgccagtcggcaggtgaccgttcctcgggagcacttc
cgcgtcatcctcggcaagggtggccaacggctgcgcgaaatcgagcgtgttactgcgacgcgcatcaacatccccagccagag
cgatgagagcgagtttatcacgattgccggaaccaaggagggtattgcccaggccgagcaggagatccgtcagctgtcagccg
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aaggacgcggtcgcagcggcaaaggccaaggtggaggccatttacaaggatatggaaaagaagtgctctaccgtcagtgtgga
ggtagctaagcccaagcaccgatatgtcattggtccgaagggctccaccatcgccgagattctgcagttgaccggtgtgtctgtag
agatgcctcccaatgactccccctcggagacgatcactttgcgtgggccgcaagtggctttgggaaatgccctaaccgttgtctac
caaaagtccaactcggtcaagtctgtggagatcaatgcggcacattggatccacaagtatgtgttcggtcgcaagggggccaaca
tgaagcagctggaggaggactgccccaacgtgaacgtgaattgcctggaagacaagatcaagctggagggagatcccgagaa
cgttgacagggctgtagcctacttgtccgaaatcatcaaaaactacgaggagaacttcacattcgaggtgatgacggttaatccttc
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cgcgagggccagaacaacatccgtatcgagggtcccaaggagggagtacggcaggcgcagcttgaattacaagaaaaaatcg
acaaactggaaaacgaaaaatcgaaggatgtgatcatcgaccgccgtctccatcgttctattatcggagctaagggcgagaagatt
cgcgaggtgaaggaccgctaccgccaggttacaatcacgatacctacgccccaggagaataccgatattgtgaagctgcgcgg
acccaaggaggatgtggacaagtgtcacaaggatctgcttaagctggtcaaggagattcaggaatcgtcgcacattatcgaggtg
cccatctttaagcagttccacaagttcgttattggcaagggcggcgctaacatcaaaaagatccgcgatgagacccagactaaaat
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tccaaaagattcaaaacgagctttccgacattgtcaccgaggaggtgcaaatcccgcccaagtactacaactcaatcatcggcact ggcggcaaactcatctcctcgatcatggaggaatgcggtggtgtttctatcaagttccccaacagcgactccaagagcgataaggt cactattcgcggtcccaaggacgatgtggagaaggctaaggttcagctattggagctggccaacgaacggcagctggcttccttt accgccgaggtgcgcgccaagcagcaacaccacaagttcctgatcggcaagaatggcgcttctatccgtaagattcgcgatgcc actggtgcccgcattatcttcccttcaaacgaggacactgacaaggaagtgatcaccatcattggcaaggaagaaagcgtaaaga aggcccgtgagcagctggaggcgatcatcaaggagtgcgacgaagtaaccgaaggtgaggtttctgtcgatcccaagcaccac aagcacttcgtggccaagcgtggcttcatcctgcaccgcatttcggaggagtgcggcggcgtgatgatctccttcccccgtgtcgg catcaactccgataaggtgacgatcaagggtgccaaggactgcattgaagcggcccgccagcgcatcgaggagatcgtcgccg atctggaagcgcagaccaccatcgaggtggtgattccacagcgtcatcatcgcaccatcatgggcgcacgtggatttaaggttca acaagtcacctttgagttcgatgtgcagatcaagttccctgatcgtgatgccaccgaacccgtcgagggtctgaccaacggaggc agcggagagaatggaggcgagaatgaaggccaggagggagagcaggaagtagagaaggaagccgaacaggagccggttc gtcagtgcgatgttatccgaatcacgggcagaattgagaagtgcgaggccgccaaacaggctctgcttgatcttatccccatcgag gaggagttgtcggtgcctttcgacctccatcgtaccatcatcggaccgcgcggtgccaatgtgcgtcagtttatgtccaagcacgat gtgcacgtagagctgccacctagtgagcttaagtcggatgtgatcaaggtctgcggtacgcccgctcgcgtcgccgaggcccgc gaagcgctggtgaaaatgattgaggattacgaggctgatagggccgatcgtgagctgcgctcctttgttctccaggtggacgtaga tacggaattccattcgaagctcattggtcgtcatggcgctgtgattaacaagctgcgtgccgatcacgacgtcatcatttcgctgcct aagcgggatgaacccaatgaccgcatcatctctatcaccggctaccaggccaatgcggaggcagcccgcgatgccatcctaga gattgttggcgaccccgagacacttcatcgcgaggttatcgagatcgataaacgcatccacccccacctcattggccaacgccga cgcaccattcgcaagatcatcgaggataataaggtgaacatcaagttctcagctgatgatgacaaccccaattcgatcttcatcagt ggcaagatagaggacgttgagaacgtcaaggagttgctcttcggcatggctgaggactacgagcgtgactacttggataacgtg gcgatagcgccgccaacgattggtgccttcctaactgggttctggatccgatgccgcaggtgccagcgagaacggattcgtcatc aaagacgcaccgtgggagaagcaaaagcaggccaaaaacctgactgcgcccaacactcagtcgcaggaggacttcccgcact tcgctgctggcggggctccggtggcctccacgcctatcacctccgtgtggggccccaaaaactaagtgcatcgggccgagtgtc ccgatcgccagcagtagcagcaatactacaagtcggggtgcgccggggatcggagctggagatggaccaggagctggagca gaagctggaactggaacttgaattggattatcgggcaatgagcggcagagcagcggcagtcgtgcggacatctctttag

***Drosophila* Gene Hit** BLASTN with rescue sequence 1: dodeca-satellite protein 1 (DDP-1) (AJ238847). TBLASTN with ORF2:dodeca-satellite protein 1 (DDP-1) (AJ238847).

***Drosophila* EST** GH20785 (AI389573), LP07358 (AI294065)

Annotated *Drosophila* genome genomic segment AE003799

Annotated *Drosophila* genome Complete gene candidate CG5170 - Dpi dodecasattelite DNA binding protein
CG5576 - Bg5 involved in cytoskeleton organization and biogenesis which is putatively a componentof the plasma membrane

Human homologue of Complete gene candidate CG5170- 4885409 ref|NP_005327.1|pHDLBP| high density lipoprotein binding protein >gi|2498434|sp|Q00341|HB

	CG5576- 2e-07 4506539 ref|NP_003795.1|pRIP| UNKNOWN >gi|3426027 (U50062) RIP protein kinase [Homo sapiens]
Putative function	CG5170: DNA binding protein (homology with Scp160p, a new yeast protein associated with the nuclear membrane and the endoplasmic reticulum, is necessary for maintenance of exact ploidy) CG5576: death domain containing protein, possibly involved in signal transduction
Confirmation by RNAi	CG5170: Reduced G1 and G2/M peaks indicating fewer cycling cells and more polyploidy CG5576: Loss of G1 peak

Example 63 (Category 5)

Line ID	40/2
Category	2nd chromosome, small imaginal discs
Reversion	NR
Map Position	39B

Rescue ID BamH1

Rescue Sequence 1

TTTTTGCCTCCGCTTTTTAATTAAAAAAATGTNTGTTTNGCCCTGGAGCTCTCG
GTCTGTTAGCGAGCGTTGCCACCTTTCTGCGAGCTGTTGCTGCACACTGCCACT
TTACGAACACAGCTCTGATAGCGGACAAAATACGTCAAGGCAGCGACGGTG
GGTTACTAGTGAATTTGGAACGGTGGTCTTAAGACGTACTGGTCTTTTATATTT
TCATTATTTTTTAAATTGTCGCTCATTTACCAATAAACCTTTTTACTTTTTCCTG
ATAGTCCGAAGTCAGATCAAATAGGAAGTTTCACAAAAAATTTTCATCCAGAG
AAAATACGCCGACGCTATTCGAGTTTTTTGTATTCGTTAACCGGGAAAGAATA
GTTCGAATTCGTTCGCACTTTATCGATAGTAGATTGCTATTATGGAGCCCACTA
GTAAATTAATTAAATTCCAGACTGATAAAAGCGATCAACTTTTGTTAATGGGT
TTAANTCTATAATAATNCTTAGTCCAAATTGTNTCAAAGTAGTCGATAATTTAT
AATAACAGTTTTAGATGACCTCTAGGAAATAACTAATTACCCACATNCTTCAA
GAAAGTGTTTNCAATTTGTNCTATAATTAAATAACAGTTGTATTAATTATGTTG
TNATTGTNACTCATAATACAAATTAAACAATATAAACACACATAAATAAGAG
AATTGGAATATTTTGTCTCAGATTAGATTTNCCAC

Rescue ID EcoR1

Rescue Sequence 2

AACGGGGGGCTTCCGCGNCNCCAAAACGCAATNTACCGTTCATGCTGTGAAG
CGAAAAAGAGTGGTAGCGCCTACCNTGGCATATGTAGTTAAATCCGTGAAAT
AAGTGAATAAGAATATATGTATGTACTTAATTCGAAAACCTTTTCGCCGTCAG
CACAACGGGTGAACGAGAGAGCGGAAGTGGAGTTTTTTGTGGCGGGTCGTCT
CGCTCGCACCGCAAANGTCGTCCGTGGCTGCGTGTATGGGTGTGTGGAAAAA
GCGTCGAGGTGAATGTGGATTTCTAACCACACCAGCATTGCAAAGACATTGAT
TGATATTTAAAGCTGCAGCAGCGAACAAAGCAAATCCTAATTTCGGCAAAGTT
TAAGAATAACGAGTGACTGGGGCGCGCGCAATAAGATAAAATTGAAGGTTAT
CTGTGTGCGTGTGAGTGACCGTNTACCAGTGTGTGTGTGCGANCGTCCATTGT
AAACAAAAAACAAGTGTTGTGAGCGGAGAGAAGAAAGGGAAAGAGAGAAAG
AGCGAACAGACTGGCGAGAGAAAAAAGAGATGCCACAAANAAAGCAGCGCA
CAAAGGAAAGCTGAAAATTTCANTAAATCTGCAAAAGTGAAGAAAACCACAA
GAACCCGCAGTCNTGTTAAATAAAACCCAGANTCCAAGAAACNTTAAAAGAA
GCAGTGCAAACAAACTGGTGCTNTGAATGCGGTTTATTTTGAAAAAAAATGCA
ATTCGGTCCGATGGAA

Genomic hit, Accession No. CSC:AC014744

***Drosophila* EST** several including LD46342 (AI544109 BLASTN similar to mRNA L07550)

Annotated *Drosophila* genome genomic segment	AE003669
Annotated *Drosophila* genome Complete gene candidate	CG8678 - novel with ankyrin homology
Human homologue of Complete gene candidate	CG8678 -gi7661580 B69CEC399B56F35C |ref|NP_056425.1|DKFZP434J 154 protein [Homo sapiens] (2.20E-85)

Putative function Novel protein with ankyrin domains, unknown function

Confirmation by RNAi Reduced G1 and G2/M indicating fewer cycling cells

Example 64 (Category 5)

Line ID 55/12
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 49C

Rescue ID BamH1
Rescue Sequence
TCTCATGNTCAGGGGGCCTTTACNATGTCAAAGAGCAAATTGTCCACAGGGCA
GCAACCGCAAGTGAGAGACGGGTGGAAAACTGGGCGGCATGACCATGAATGA
AAGCCGCGACCGGCAAACGTGGCCCGCCCACAAAGCGAGCATTTTCACATTTT
AACTGTCTGGACATTTTGTAAGTTACACCAAGGCAATGATACCAGTAAAAAAG
AAGAAACAATCATTTTTGAATAGATTAATCACCTGATTAATGTTGGTTGTATGT
TGATTGTAGGTGTTTTAATATACAATGTCTCTATTACTGCTTTCCTTTATTCAAA
AGCCATGTGTAAGTGTAAGTTCTCGATTTCGGCTAGATTTTGAAGTTCTGCCAT
TATCAATTAAAAGTCCAGTTCCTCTATAAATTGGTAATAAAATAGCTCTTTACA
GCCAAGTATATGTGCAATTTTGTAAGATTAAANGTCCAAATGTTGTGAACCTT
TCCTGGCCCTGAATTTTAAAAAACCATTAAATTGGTCCCATTTGACATTAAATG
TTCTATGTACATTAATATGACTTTTTGTGGATGGTTTTATAAACAAGCATTACT
ATATTCTAAAAATCAAGGATAAAGGACNAGCTTTACAGGAGGTAACATTCCTA
TTGTACGGCTTTATTTTCTTATACCCATAAGAGCATACCACTAGGATCCGTCGA
CCTGCAGATCTCTAAAAACTTGCCTTTGCTGGCGTTTTCCATAA

Genomic hit, Accession No. AC007085

Associated ORF
Genscan ORF1 predicted sequences >21:54:11|GENSCAN_predicted_peptide_3|108_aa
MGLVTAAFKLKRKDIQDRYQHDINRICHTRSTAHTAYAHFAEHLLRRSPRQRFVN
GKGAALVLILLVSAARQFSGSTGAYKLGNRVGKVEGEQQEYKLQDRTTHFCGN

>21:54:11|GENSCAN_predicted_CDS_3|327_bp
atggggctggtaaccgccgccttcaagctgaagcgcaaggatatccaggacagatatcagcatgatattaaccgcatctgccaca
cacgtagcacggcacacacggcgtatgctcattttgcggagcatctgttgcgacgaagtccacgtcaacggtttgtcaacggcaa
aggtgctgcgcttgtgctcatcctcctcgtttctgcggctcgacaattttctggctcgacaggtgcctacaaactgggtaatagagttg
gaaaagtagaaggggaacagcaggaatacaaactacaagacagaacaacacatttttgtggcaattaa

Corresponds to CG8732

Annotated *Drosophila* genome genomic segment AE003836
Annotated *Drosophila* genome Complete gene candidate CG8732 - l(2)44Dea homology to fatty-acid-Coenzyme A ligase, long-chain previously described spindle/chromosome

	abnormalities in neuroblast squashes
Human homologue of Complete gene candidate	1e-171 4758330 ref|NP_004448.1|pFACL3| fatty-acid-Coenzyme A ligase, long-chain 3 >gi|4165018|dbj|BAA371 and LCFD_HUMAN LONG-CHAIN-FATTY-ACID--COA LIGASE 4 1e-157

Putative function Fatty acid CoA ligase

Confirmation by RNAi Only wild type profiles observed

Example 65 (Category 5)

Line ID	6/7
Category	2nd chromosome, small imaginal discs
Reversion	NR
Map Position	28E

Rescue ID BamH1
Rescue Sequence 1
TATNAATAATCATAGGGCTCTTGCTCTTACGTGTAAGGCCTGCCCCTCTNCCA
GTCTATATACAAAGAAAAACACACACACACTGGCACACTGGTGTTCGCATATG
CCAAAGCCGAGTTAATTTCACTTTGTTTAATCTATCGTTTGGTGTTTTTGCATTT
TTTAACCGCGCAAACGGTATTTGCGCGTTTTGCGCCTCTTACTTTGCGATTTAT
TGCACCGCTTGGCTGTGTTTTGCAATTTCTATCTTGATTTTCATTGGTATTCACG
CGTAATGTAATTCTTAGCAGCGTGACCGCGCCGATAACGATAAAAAATACCAC
GGGACCAAAAATAAATACCATATGATACCACTTCAGGGAAAAGAAATCCTAT
TTAATACCACTCACTTTAAAAATAAGTTTTTAAAAATATATATNTTTATTTAAA
AAAAGGTGTATTTATAATCAAATACTCGGTACTTNTTAATTACTCCAAGAANA
ATTAATTTGAAAAAAAGGGGTTCCATTATAAAATATATATTAACCGCTTACAC
ATAATCCCCAAACAAAACAGCGATTGGGATTTAAAAGGTTCTAAGTCCATCAT
TATAAAAGATCATTTCCGAAAAACAAAAGAAATAGATTCAAAATTAGGCGAC
ATCAGCCCGCTGATAANGATCATAAAAATACAGAAGCTNATTCAGCGAATCA
GAAANTCCTACTCGCCACTATCCGAAAACNTNGAAAAAAAATGG

Rescue ID EcoR1
Rescue Sequence 2
TGAAAGGTAGCAACAACGTTTCCTTGGAAAAAGCTGTAAATAGTAAACAAAA
TTGTCAAGTTAACGAGCCAAAGTTATTAAATAAGGTTCGAGTACGTTGGCATC
GGCTGCCCAGGCAGCAAANAAAAACAAAGACGCAGTTCAAGATCAGCTGGAC
ACTTAGAAGANTTTAAGAATTGAAGCACATTNNAAAGAAGANAAACAAGAAC
CCCACCAAAAACCCGCGTGCGTTTGTATGTGTGTGTGCCATCAAATTTCCCGC
ACTGGGTGAATGTGCNTGCGTGTGTTNTGTGTCATTTAATTTTCCTACCAATAA
TCGCCTTCCAAGAAGTGAATACCAGCCGATCCACCGCTAAATCGAAAAAAGTT
TNACTCTGGGTTAANTCACTGTTTACGGCTTTTGTGCTATAATTACCTTTCCCG
TAAGCNGTGGGAANCTAAAANCCAAAACNTNAGAATCCGAATTCCG

Genomic hit, Accession No. CSC:AC017934

Associated ORF
Genscan partial ORF1 predicted sequences
>22:35:21|GENSCAN_predicted_peptide_4|128_aa
MGTNSGATAGINNKPVGGATGAGVLVGGGVGGANSSIGGVLSNSLGGGGSGGLS
ISGLNAGGQNANVGGMGNVGGDDGGNGMVGGGVNNQQATTPQYTIPGILHFIQ
HEWSRFELERSQWDVDRAELQ

>22:35:21|GENSCAN_predicted_CDS_4|384_bp

atgggcaccaattcgggagccaccgctggcataaacaacaagccggttggcggtgcaacaggagccggcgtccttgtaggcg
gcggtgtgggcggtgccaattcctcgatcggcggtgtcctgtcgaacagcctgggcggtggcggcagcggcggtctgagcatc
agcggcctcaacgctggtggacagaacgccaatgtgggcggaatgggcaacgttggcggcgacgacggcggaaacgggatg
gtgggcggcggtgtaaataaccagcaggccacaacgccccaatacacaataccgggcatcttgcacttcatccagcacgagtgg
tcgcgcttcgagctggagcgatcacagtgggacgtggacagggccgaattgcag

Human Homologue	TBLASTN with ORF1: very weak homology with striatin, calmodulin-binding protein (STRN) (NM_003162.1)
***Drosophila* EST**	several including LD42534 (AI516610), LD03224

Annotated *Drosophila* genome genomic segment	AE003619
Annotated *Drosophila* genome Complete gene candidate	CG7392 – novel WD40 family member

Human homologue of Complete gene candidate	CG7392- SG2N_HUMAN CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 ... 622 e-178 A cell-cycle nuclear autoantigen containing WD-40 motifs expressed mainly in S and G2 phase cells

Putative function	WD40 protein a novel nuclear protein mainly expressed in S and G2 phase cells that was characterized using autoantibodies from a cancer patient

Confirmation by RNAi	Reduction of G1peak , more polyploidy

Line ID	103/1
Category	2nd chromosome, small imaginal discs
Reversion	R
Map Position	57B

Rescue ID	BamH1

Rescue Sequence 1
GATTTCAAAATTAGGCGACATCAGCCCGCTGATAAAGAATCATAAAAAATACT
GAGGCTTATTTTAGCGAGTCAGAGACTCCTACTCGCCAACTATCGAAAACATA
GNGAAGATATAGTCGCCAACCGATCTGCCTTCTATAGTGTTGCTTATTGTTGTC
CCCTAATCAAATTAATAAAAATCTGCATTAGGCTGCTTCGCCGGCCAGCAACA
AATGTTTTACACCTACTGTACTTTTCGCAGAACAGAGATCCAAATGCAGGATC
GTTTCCATGACTGTACATTTATTCGGATTAGACATTAAATTACACCCTACAGCT
ATACATACTAACAGTGAACACGGCAAATGCTTAGCTAGCATTGGGCCACTTTC
GTTGACTGCGAATAAAAATGATTGGCCGATGCCTTTAGCAGATTCCTTTTGAT
CGAATTACTCGGATGGCTTGTGTGTCCACCTCTTACAAGAACTCCTCGCACCA

ATCGTTGAGACAGTTGTAGCAATCGGATGCTTGGTTGGAGCTGGCGTGGCACA
CCTTCTTCATCCAGTCCTTGGACAGNTTCTTGGNCCTTTTCAGNANCAGGATCT
GGTCCCAAACGGNGGAAGGCCTAAAACGAATGGNAATTGATCGGTAGCCCTT
GACTGGCATTGGTAATTTGCGCACATGGGNGTCATCGGATTTACACACGCACC
ATATCGAATCAGCGTCCTTAAGCGTCAACCGAGGGTTTCCCCAATTCCGGCCA
GTTCCGTCACCGACTTGGTTGCCATTGG

Rescue ID EcoR1
Rescue Sequence 2
ATCAAAGCGNCTGGGCCCGTGCATCGCCNCAGCGTTCGTCTTAATTAATTAGT
GATTGCAAGCGGGTGCAATTATGCACAAAATTACGGACTAATACAACTGCCC
GCTTCGCGCTCTCTCCATCTCCCTTCCAAATAGTCGTTTGCTCTTCGCACACAA
AAGTGTAAACCCTGTGAAAGGTAGCAACAACGTTTCCTTGGAAAAAGCTGTA
AATAGTAAACAAAATTGTCAAGTTAACGAGCCAAAGTTATTAAATAAGGTTCG
AGTACGTTGGCATCGGCTGCCCAGGCAGCAAAGAAAAACAAAGACGCAGTTC
AAGATTCAGCTGGACACTTAGAAGAGTTTAAGAATTGAAGCACATAAAAAAG
AAGAGAAACAAGAACCCCACCAAAAACCCCGCCGTGCGTTTGTATGTGTGTG
TGCCATTCAAATTTCCCTGCACTGGGTGAGTGTGCGTGCGTGTGTGTGTGTC
AGTTTAATTTTCCTACCAATAATCGCCTTTCCAAGACGTGATTACCAGCCGATC
CACCGCTTAAAATTGATAAACGTTTTAACTCTTGCGTTACATCAGCTGTTTTAC
GGCTTTTTGTGCTATAAGTTACGCTTTTCCCGTAAGCCGTTGGCAACACTAGAA
CGCAAAAGAGCATAAAGAATCGCGAGTACCGTANAGAGGAAGAGAGGAAGA
GAGAGAGATAGAGAGTGTGAGCGTGTGAGTGAGCGGGGAATGTGGGGGCGGT
TCCGGTGCGAAAAAACGTAGTAGTAGTACATNNAGAGAGTGCGAACGAGAGG
GAGGCAGCCAGCGAGTGTCCTGCGACTGCTCCCCCCTTTACCCTCGTCGCTTTT
CTATTCGGAAAATTCAATGACCTCATTTGTTTCATGTGCCGAACTTTGCTTTTC
TTTCCCAACCTAAAAACGCAAAAAAAAAAAACNCCAAACAGGATATACGTNG
GAACANTGANCAAACNANTTCGANAAAACCAACAACNANGGACCGTGCCCTG
GGGCNCCTGAAAGGCAAACAGCTGGCNNCAAATCCGGAAAAGGATCNGGAA
NAACAGGATCNGCGGGCNCAAGGATCNCCGGAACAGGCAAAGGAAACNCCC
GGCNCACNGCACAAGCCNCTGAAAAGCAACNTGAACCAATGGGCACCANTTC
CGGGANCCACCGCTGGCATTAAA

Genomic hit, Accession No. CSC:AC017934

rest of results as for line 6/7

Example 66 (Category 5)

Line ID 65/24
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 48A

Rescue ID BamH1
Rescue Sequence
TACGATTTTTGCANTGCNCCATTTCGTGGCACCCGATTTGTATATATATTTTTT
ATATAACCCACGGATTGCCAACTTTCATTGCCCTTTCACACTCTTATTCGCCAT
TTATGAACTCTTCTTTGACGATTGGAACGGTTCTTTTTCGCTATTTTCGACTGC
ACCCGCGCTCTTTTCGCTTCGCTCTCCTCCCTCTCTACACACCGCTCTTTATCCT
TAATTGCTTTTTCTATTTAGCGGAATTGATCGTTCTCAACTTGGTCGCCATTGC
AGCTCCACAGGCGAAAAAATCGGTGGAAATGCCAATACAGGTGCACGGCGAG
TGCCGATAAGCTGGAAAATCGGGAAAACGCACGCCTACACATTCATTGCCAG
CATCGGCTTTGCCTTTTCGCTGTCGAGATTAGCATATTTCCACTTTTGGTTCGC
GCACAACACTANCTAAATTATTGNTTATTTTTTTCCCCAACTGTGAGGTGAAAC
TGTGAAACAAAACCACTGTGGGCGGGTCAGTGTGACCCTCTCGCGGTGGGTG
AAAATCCTAGTGAGCTTCGTTGTTAGGGCTGTATGACACGAAAGCAAGTTGAA
AAGAAACTTTTTTAAAATTATATTGGTTAATTGAGCAGAACTAAAACTATATN
AAAATATTTAAGAATNCAGATTAGTGATGTATTTAATATAATAATAGTAAGAT
GTTC

Rescue ID EcoR1
Rescue Sequence 2
CTTNTTTGATAGANATAGGCTTCTTTTAAAAAAAAANAAGCAGCANCAGGGG
CCCNGAAGTGCGTGNNTGTGAACGCTGATTGCTTGCAAGTGTGTTCGTGTGTG
TGTGATTGTGTGCTCCGANCAAGTGAAATCAATAATATTTGCAGCCACAAGCA
ATTAATAAAAACTGCAATAATGTCAAAAAATCTAATTGAGGCAACAAATTAN
CAAAGCCATNAAAGCAGGCTGCACTGCGAGAAAATTGTGCCTTTCCACAGAT
CTTCTGCTGCAAAGCNAAAGAANGTAAGCAAGTCGGCCANTTTATTNCATTCT
TCTCATCTCTCTTCTTCGCGAATTGGCGCNTANCACTTACAATAATTNATATNA
CTTCTTAAATTTCAAANTCCCTTTCNTGAACGGANCTTTTAACGGAAAACAAA
GCGGGTAAACTAACTTAACTAAACTAATTANAANTGTANGTATAAATGAACC
GAACTCGCTTTAGATATNATGCGTTTCACTAACANATTANAACAAACTTTGAA
GCTGTANTGTCAGGTTGTTATTNCGTTCACCANATGTAGACTGNCCGNNAATT
TNACCTTTCCCATANTCTGTTCTTAANTGTNTTGTTTTTTCCCAATNNTTTGATC
ATNCNTTGGTNAATNANCTNAACGGCCCAAAGTNAATGAATTCCANTCACGTC
CACTGGCTCTGGTTCNATANTTAATNGGCTGTTTCTTACTTCCCTTAACCCTAA
CATCTNTTAATCACCTGTGCCATNTGTTTGTGTGTGTGTGAACGAATGAGAAA
AAAAA

Annotated *Drosophila* genome genomic segment AE003825

Annotated *Drosophila* genome Complete gene candidate	CG9005 - novel putative cell adhesion
Human homologue of Complete gene candidate	CG9005- Ensembl predicted gene ENSP00000006008 Gene:ENSG00000005238 Clone:AC004472 Contig:AC004472.00001 6.00E-38 (KIAA1539 protein AB040972) and AK022837 Homo sapiens cDNA FLJ12775 4e-33
Putative function	Putative cell adhesion protein
Confirmation by RNAi	Reduced G2/M peak

Example 67 (Category 5)

Line ID 74/3
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 47A

Rescue ID EcoR1
Rescue Sequence
GCACAGAATGGCNCCTTCACGACAAAAGATCTNCNAATTAGGATGATGCAGA
AGGAGGACACGCTTTTCATTATCTGGTTGCCACCTAATTTAAGTTCCACATCAA
GGGAAGAAGGAAATACGTTCCAACGGACGTCAAATTTACTAACTACACTACTT
GAAAAGCCTGTCTATAAAAACACGATAACGTTTTTGCTAATCTCAAGACAATG
TTAAATATAATTGGAGAAAGTATTGAATATGAATATCACAAAAATTGTTTAGG
GTCTCTACGTGGTAAATAGTATTTGGCATAGACAGTGAGATGTGAGTCGTACG
TACTAATTAATAAAGTTGTTCAARAGAACCTCATATACTGTAAGTGACAACGA
ACGAAGCTGACAACTCTGCTTGCACATATTTGGCGGAGTTCGAAAATATCATC
GCATTGGTATTGTTTTTGTNTCCACCNTGGGGCGAGATTTTGTTGTTGCTTTAC
TTTGCTTGTTTTTTCNCCACAAANCGAACCATAATGTTCGAAATGGTAAAATTA
CCGTGCCAACAAGCTCTCTCTCTCCCCACTCCGAAACTCTCTCATCTCTCCTTG
CAATTGTTTAAGGTGTGCAAGGAAATGAAAAATGTCCCGGCTGTGTTNCCATG
CATTCCCCTTCAAAGCCAATTATNTTTGTGCCTCTCCAACNTTTTTGATCGGNN
TGATTTTTTTGGCTCCCCNTANTCCCCCCCCCTTTCNCCCATTCCGGGTTANAT
TATTNTNCCAATTTTCCTATTTTACGGTCCCNGTTCCCTGGAAATANTTCCTNC
AATCNCCGCTCCATNTCNCCATNTTTGACAGATTTTC

Annotated *Drosophila* genome genomic segment AE003829
Annotated *Drosophila* genome Complete gene candidate CG12052 lola -a specific RNA polymerase II transcription factor involved in axon guidance

Human homologue of Complete gene candidate 1e-09 3789797 (AF059569) actin binding protein MAYVEN [Homo sapiens]

Putative function lola-like specific RNA polymerase II transcription factor

Confirmation by RNAi Almost no G1 peak and increase in G2/M peak indicating arrest in G2/M

Example 68 (Category 5)

Line ID 79/7
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 55B

Rescue ID BamH1
Rescue Sequence 1
GTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGTGTGC
GAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCGTCCGGGGTTAT
CGGTAGCTTCTTCTAGGCTGAGTGCATTTCGTTGAATCGTGGATGTTGAAAGTT
GTCTAATTTCCGAACTATTGATTTTTCCCCTTCCCCGTCAAGAAACTGCATTGT
TGCTTCTTGAAGACCAGTTTTGGTAACATCAGGAGAATGGAAAGGAGCGAGT
GAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACAACA
ACAACAACGGTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAACAATT
TGAGCAGCTCCGTTTGTTGTTATTGCATTACTCAATCGGGAAGACTCTACACTC
GACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCCTTCCTTTGTTT
TTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGAACCAC
CAAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAATATTATT
GTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTCATATAC
ACGCAGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCCGTN
CACATACACTTGTCTTTTTNCCACACACTTTCCTAATCAT

Rescue ID EcoR1
Rescue Sequence 2
NGGNGTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGT
GTGCGAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCGTCCGGGG
TTATCGGTAGCTTCTTCTAGGCTGAGTGCATTTCGTTGAATCGTGGATGTTGAA
AGTTGTCTAATTTCCGAACTATTGATTTTTCCCCTTCCCCGTCAAGAAACTGCA
TTGTTGCTTCTTGAAGACCAGTTTTGGTAACATCAGGAGAATGGAAAGGAGCG
AGTGAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACA
ACAACAACAACGGTTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAAC
AATTTGAGCAGCTCCGTTTGTTGTTATTGCATTACTCAATCGGGAAGAACTCTA
CACTCGACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCCTTCCTT
TGTTTTTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGA
ACCACCAAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAAT
ATTATTGTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTC
ATATACACGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCC
GTNCACATACACTTGTCTTTTTNCCACACACTTTCCTAATCATNNTA

Genomic hit, Accession No. AC004296

Associated ORF
Genscan: ORF2 predicted sequences >15:31:31|GENSCAN_predicted_peptide_3|109_aa
MVTSFRHLRDEKSFTDVTLACEGQTCKAHKMVLSACSPYFKALLEENPSKHPIIIL

KDVSYIHLQAILEFMYAGEVNVSQEQLPAFLKTADRLKVKGLAETPSSIKREG

>15:31:31|GENSCAN_predicted_CDS_3|330_bp
atggtgacctcgttccgtcacctgcgcgacgagaagagcttcacagatgtaacactcgcctgcgagggccaaacctgcaaagcc cacaaaatggtgctttccgcttgcagtccctactttaaagcgctactggaggagaacccatcgaagcatccgatcattatcctgaaa gatgtctcctacattcacctacaggctatactggagttcatgtacgccggtgaggtgaacgtgtcccaggaacaattgccagcattt cttaagaccgccgatcgcctcaaagtgaaaggcctcgcagagacacccagttcgataaagcgggaaggttga

***Drosophila* Gene Hit** TBLASTN with ORF2: several zinc finger proteins including Broad-Complex mRNA for BRcore-Z2 protein (X54665)

Human Homologue TBLASTN with ORF2: kelch (*Drosophila*)-like 2 (Mayven actin binding protein) (KLHL2) (AF059569)

Annotated *Drosophila* genome genomic segment	AE003800
Annotated *Drosophila* genome Complete gene candidate	CG5738- lolal, lola-like putative kelch-like putative specific RNA polymerase II transcription factor known to affect disc morphology or could be CG10914 - novel unknown
Human homologue of Complete gene candidate	CG5738- 9e-09 3789797 (AF059569) actin binding protein MAYVEN [Homo sapiens] CG10914- predicted gene ENSP00000051207 Gene:ENSG00000047313 Clone:AC068261 Contig:AC068261.00019 4.00E-49 (potental cell division GTP binding protein 1: ENST00000051207

Putative function CG5738: lola like specific RNA polymersae II transcription factor, CG10914: Possible GTP binding protein

Confirmation by RNAi Both show marked reduction in G1 to G2/M ratio

Example 69 (Category 5)

Line ID 80/2, 81/8
Category 2nd chromosome, small imaginal discs
Reversion R
Map Position 57D/E

Rescue ID BamH1
Rescue Sequence 1
CANTTTCAGAGGCCATAGNCCTTCACAAAATTCNCCATCTCTGCCCGGCATCC
GTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCACTCGATGGTC
TGCAAAATTGCACATTTATTAGATTTAATAAATTTTTCAACTGTCCGCGANCAC
GTTTGCTCGTGTTGAATTTCGAGTACAAAATTAGTGCGACTGTTGGATTGCATT
GAAATGCCAAAAATCGGTGTGACCATTTCGAAGTCCCCACAGGCTCATGACTT
TCGCGGTTCACCAAATCCAAATAACGCAAGCTGGTCACGCTGTCAAACATCGG
TGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTTCTTGCGGCCGT
AAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACGTAATTGGAACA
AATGTTTGCTGAACCACAACCGCCCACTAAATGTTANCCGCCAAGTCTTTTCC
CCCGCCGCCGCCGTCNTCNTCNTCNCCGGATTATTTGGTTTACAATTTGCTTAC
ACAAGTGCAATCGTCGATAGCGCTTCATTTTGGAGTAACAAGTAATATTTTGC
GCCGTACTGCTGTTCGCCGTATCAGACAGAAGGTTGGTATCAGTTCGACGCAG
CTTGTGACGGTATTGCATACGCGGCGAAACGCCCACGTGAAAACGGATCGCA
GTTCTCGAAAACTCNGGATAAAAA

Rescue ID EcoR1
Rescue Sequence 2
TGGGGTCTCANGCCCCGACGGCCATATTTTAACACAAGATTCNNCANCTCTGC
AGGGCATCCGTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCAC
TCGATGGTCTGCAAAATTGCACATTTATTAGATTTAATAAATTTTTCAACTGTC
CGCGAGCACGTTTGCTCGGTGTTGAATTTCGAGTACAAAATTAGTGCGACTGT
TGGATTGCATTGAAATGCCAAAAATCGGTGTGACCATTTCGAAGTCCCCACAG
GCTCATGACTTTCGCGGTTCACCAAATCCAAATAACGCAAGCTGGTCACGCTG
TCAAACATCGGTGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTT
CTTGCGGCCGTAAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACG
TAATTGGAACAAATGTTTGCTGAACCACAACCGCCCACTAAATGTTAGCGCCA
ACTNCTTTTCCCCGCCGCCGCCGGTCGTCNTCNTCCCGGATTATTTGTTTACA
ATTTGCTTACACAAGTGCAATCGTCGATAGCGCTTCATTTTGGAGTAACAAGT
AGTATTTTGCGCCGTACTGCTGTTCGCCGTATCANACAGAAGGTTGGTATCAG
TTCGACGCAGCTTGTGACGGTATGCATACGCGGGGAAACGCCACGTGAAAAC
GGATCGCAGTNCTCGAAACTCNGGATAAAAGAAAAAGTAGGCTGAATG

Genomic hit, Accession No. AC007175

Associated ORF
Genscan: ORF2 predicted sequences >16:09:09|GENSCAN_predicted_peptide_3|2497_aa
MNEGNSAGGGHEGLSPAPPAVPDRVTPHSTEISVAPANSTSTTVRAAGSVGAALP

ATRHHQHIATQVKGIASSSSKQQKQLASAQLPVPLSPLPQQQQQTAEATAAAAAP
AHSNVSVSSSTIEASVLPPQAKRQRLDDNEDRTSAASIVGPAESSNIVSSLLPASVA
SSSEVGGLSSTALQDLNALKKRILQQKLQILRNLKERHLENVSEYFYLQNGGSMM
DYPAWRKKTPTPQFISYSNANRIDQLIHEDKPSTSAAAAAAQNQKYTTQQTDSVE
SSLVSGIGTGATKGAPLDGNISNSTVKTNTQSQVPSKIGSFTESTPAATESNSSTTVP
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***Drosophila* Gene Hit** TBLASTN with ORF2: brahma protein (M85049) and imitation-SWI protein (ISWI) (L27127) and chromodomain-helicase-DNA-binding (CHD-1)

Human Homologue BLASTX with EST TBLASTN with ORF2: Snf2-related CBP activator protein (SRCAP) (AF143946) and SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4) (NM_003072.1)

***Drosophila* EST**	several including SD07794 (AI534784), LD34465 (AA990657)
Annotated *Drosophila* genome genomic segment	AE003453
Annotated *Drosophila* genome Complete gene candidate	CG9696 – domino an enzyme involved in DNA repair homology to snf2 family helicases
Human homologue of Complete gene candidate	CG9696- gi4557447 416409C913D6A935 |ref|NP_001261.1| chromodomain helicase DNA binding protein 1 [Homo sapiens] (1.90E-85
Putative function	snf2 helicase family member protein that contains a chromodomain, which occurs in proteins that are implicated in chromatin compaction, and an SNF2/SWI2-like helicase domain, which occurs in proteins that are believed to activate transcription by counteracting the repressive effects of chromatin structure
Confirmation by RNAi	Loss of G1, peak,increae in G2M indicating arrest in G2/M

Example 70 (Category 5)

Line ID 99/31
Category 2nd chromosome, small imaginal discs
Reversion NR
Map Position 53E

Rescue ID EcoR1
Rescue Sequence 1
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Rescue ID BamH1
Rescue Sequence 2
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Genomic hit, Accession No. CSC:AC020063

Associated ORF

Genscan ORF1 predicted sequences >16:48:25|GENSCAN_predicted_peptide_1|722_aa
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Human Homologue TBLASTN with ORF1: poor homology with DEK gene (D6S231E) (NM_003472.1)
***Drosophila* EST** several including LD33301 (AA979048)

Annotated *Drosophila* genome genomic segment	AE003805
Annotated *Drosophila* genome Complete gene candidate	CG5935 - EG:EG0003.6 - novel with weak homology to DEK oncogene CG8648 - EG:EG0003.3 - novel XPG/ flap endonuclease-like, DNA repair?
Human homologue of Complete gene candidate	CG5935- 1e-17 4503249 ref|NP_003463.1|pD6S231E| DEK gene >gi|544150|sp|P35659|DEK_HUMAN DEK PROTEIN >gi|284375| CG8648- 4758356 |ref|NP_004102.1|pFEN1| flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN(aa)

Putative function CG5935: function unknown but putative DNA-binding protein predicted to be involved in chromosomal organisation. The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA
CG8648: Novel XPG/ flap endonuclease-like, DNA repair protein

Confirmation by RNAi Both show slight reduction of G1 peak

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Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

CLAIMS

1. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

2. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

3. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 15 to 19 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 15 to 19 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

4. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 20 to 30 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

5. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

6. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

7. A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of Claims 1 to 6.

8. A polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a homologue, variant, derivative or fragment thereof.

9. A polynucleotide encoding a polypeptide according to Claim 8.

10. A vector comprising a polynucleotide according to any of Claims 1 to 7 and 9.

11. An expression vector comprising a polynucleotide according to any of Claims 1 to 7 and 9 operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.

12. An antibody capable of binding a polypeptide according to Claim 8.

13. A method for detecting the presence or absence of a polynucleotide according to any of Claims 1 to 7 and 9 in a biological sample which comprises:

(a) bringing the biological sample containing DNA or RNA into contact with a probe according to Claim 9 under hybridising conditions; and

(b) detecting any duplex formed between the probe and nucleic acid in the sample.

14. A method for detecting a polypeptide according to Claim 8 present in a biological sample which comprises:

(a) providing an antibody according to Claim 12;

(b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and

(c) determining whether antibody-antigen complex comprising said antibody is formed.

15. A polynucleotide according to according to any of Claims 1 to 7 and 9 for use in therapy.

16. A polypeptide according to Claim 8 for use in therapy.

17. An antibody according to Claim 12 for use in therapy.

18. A method of treating a tumour or a patient suffering from a proliferative disease comprising administering to a patient in need of treatment an effective amount of a polynucleotide according to any of Claims 1 to 7 and 9.

19. A method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of a polypeptide according to Claim 8.

20. A method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of an antibody according to Claim 12 to a patient.

21. Use of a polypeptide according to Claim 8 in a method of identifying a substance capable of affecting the function of the corresponding gene.

22. Use of a polypeptide according to Claim 8 in an assay for identifying a substance capable of inhibiting the cell division cycle.

23. Use as claimed in Claim 22, in which the substance is capable of inhibiting mitosis and/or meiosis.

24. A method for identifying a substance capable of binding to a polypeptide according to Claim 8, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.

25. A method for identifying a substance capable of modulating the function of a polypeptide according to Claim 8 or a polypeptide encoded by a polynucleotide according to any of Claims 1 to 7 and 9, the method comprising the steps of: incubating the polypeptide with a candidate substance and determining whether activity of the polypeptide is thereby modulated.

26. A substance identified by a method or assay according to any of Claims 21 to 25.

27. Use of a substance according to Claim 26 in a method of inhibiting the function of a polypeptide.

28. Use of a substance according to Claim 26 in a method of regulating a cell division cycle function.